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GENESEQN: T94964
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applicant: foon, kenneth a.
applicant: chatterjee, sunil k.
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## Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (9) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

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Cor The patent discloses new catalytic antibodies which hydrolyse mano catalytic antibodies which hydrolyse mano catalytic antibodies which hydrolyse mano catalytic antibodies are mano-protected.

Also disclosed are new hybridomas expressing the catalytic antibodies, catalytic antibodies are raised in sice using the compound p-nitrobenyal (catalytic plantic) the produced are mano-protected.

Cor antibodies are raised in sice using the compound p-nitrobenyal (catalytic plantic) subjiliposphomate as hapten. They are used for efficient resolution of racesic maino acids useful cor the production of optically settive drugs and chiral separation sents.

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Cor the production of optically active drugs and chiral separation of the production of the bybridoma skalod. The Light chain of antibody 30, produced by sequence 652 BP. 194 A; 151 C; 154 G; 153 T.
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18 House monoclonal antibody B9 100, ar
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15-JUN-1995.
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Primer, amplification: FCR; mouse: Kappa chain; heavy chain; artiface marker; octal; surface marker; foetal; sequential; wastatic; therapy; Alabelmer's élassas; hybridoma; tential hyperchoseteroleenis; binding affinity; ds.

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arteriosclerotic lipoprotein;
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                                                                                                                                                                                                                                                                                                      variable region
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(ROAD ) KOREAN SCI & TECHNOLOGY NPI: 97-367067/34. P-PSDB: W27089.

REFERENCE CONTRACTOR SUCCESSION OF THE SUCCESSIO

8 8 8 8

342

282

Query Match 19.5%; Best Local Similarity 100.0%; Matches 85; Conservative

THE SERVICE OF SERVICE

signal\_peptide

ş B 8 B

Query Match Best Local S Matches 10

23.4%; cal Similarity 100.0%; 102; Conservative

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Page 30

25-App-1989.
25-App-1989.
218-App-1989.
27-App-1989.
28-App-1989.
29-App-1989.
29-App-1989.
29-App-1989.
29-App-1989.
20-App-1989.
20-A

PR 08-DEC-1993; US-164022.

PR 08-DEC-1994; US-1504002.

PR 08-DEC-1994; U

Query Match 19.5%, Score 85, DB 16; Length 723; Best Local Smilarity 100.0%, Pred No. 1.02-60; Indels 0; Matches 85; Conservative 0; Minatches 0; Indels 0;

RESULT 8

1D W91657; standard; DNA; 639 BP.

AC 891657; DT 14-MAR-1990 (first entry)

DT Chimeric antibody light chain variable region.

AW K51/4; chimeric antibody; light chain variable region

BY R51/4; chimeric antibody; light chain variable region 8 8 8 8

Mus. EP-338767-A.

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Mon

115 G; 116 T;

OUR 10

O48038 standard: cDNA to mRNA; 882 BP.

O48038;
08-FEB-1994 (first entry)
08-FEB-1994 (first entry)
Annoclonal antibody M(alpha)2-3 L-chain coding sequence.
Anti-manke small neurotoxian antibody; kappa; light chain;
Immunoglobulin; bispecific bivalent antibody; cell-targetting;
cytotoxic agent; as
Location/oun1441--Location/oun1441--signal\_peptide Location/Qualifiers

cds mat\_peptide

EP-55(111-A.

18-NGC-1993; 400323.

09-FEE-1993; 400323.

11-FEE-1993; FF-001505.

11-FEE-1993; FF-001505.

(COMS) COMPAINT ENERGIE ATOMICUE.

COMS) COMPAINT ENERGIE ATOMICUE.

EPIT-99-26(3531/3):

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mat\_peptide /\*teg b/preduct\* 1g\_light\*chain
37.354
/\*teg c/product\* 1g\_variable\_region
55.675
55.675
/\*teg c/product\* 1g\_constant\_region

RESULT
AC 088
DI 088
DI

Gaps

extra:capsular cataract extraction.

Disclosure T9, 1; 68p; Esglish.

An immunotoxin (given in R70977) comprises the heavy (WH) and light claim (VL) washabe regions of anti-tens epithelium I933 Mab 4197% linked to ricinable regions of anti-tens epithelium I933 Mab 4197% (085887-88, respectively) were obtained from hybridoma mRNA, complified by Ecg. and englishesered for inclusion in the immunotoxin construct (085386).

Sequence 405 BP; 118 A; 116 C; 115 G; 116 T;

Ouery Match Collective 19.1%: Score 83: DB 14: Length 465; Best Local Similarity 100.0%: Pred. No. 88ec-59; Matches 83: Conservative 0; Mismatches 0; Indels 0;

US-08-836-455-1.

Page 31

MON.

Αpr

PP PSDB: R40185.

PP PSDB: R40185.

PP Language Linked to dimeric proteins - with immunoglobulin pri tangents linked to dimeric protein, for diagnostic or tangents linked to dimeric protein, for diagnostic or transperts linked to dimeric protein.

Pr Language Linked to dimeric protein.

Pr Language Linked to dimeric protein and language linked from the anti-snake small conclude the protein and the protein and language linked from the anti-snake small conclude the protein and the protein smooth language linked from the same sure using children to the same vertex in the Hohaln fragment was inserted concluded in the same sure using primers (98041 and 98042. The two amplified fragments was inserted concluded the respective and the respective linked in the same sure using poles for a sequence, a signal peptide and the first is codons of photon for cassette was positioned between the tirst is codons of photon. The cassette was positioned between the first is codons of photon for the transcription termination sequence of photon. The fusion codonstruct is expected to to encode a hybrid protein companies to district a bar-derived units. The invention also covers hybrid continued proteins containing two districts hab-derived units. The invention also covers hybrid continued proteins containing two different hab-derived units. The produce of the photon, the hybrid molecules can be used as cell-targetting containing the sequence (80 MB): 231 A; 241 C; 194 G; 216 T;

F

310 taxosyttoggagggggaccaagetggaaataaaacgggetgatgetgcaccaactgta 378

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RESULT TO AC 17 AC 18 MO 18 MO

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w09503828-A. / "cay" a

0-FED-1995;
15-7UT-1994;
007-NUC-1993;
05-101399
1800TS: NOUSTON BIOTECHNOLOGY INC.
0011d RM, Kelleher PJ, Wallace TL, Wood MS;
WPI: 95-043039.11.
P-FSDB; R70828.
New adaple chain immuno:toxin - binds specifically to epithelial cells, for inhibiting development of sec. cataracts after

Location/Qualifiers 1..465 /\*tag= a

083337 standard; cDNA; 465 BP.
083337 standard; cDNA; 465 BP.
083337 standard; cDNA; region.
MAD 4397X 1914 chain variable region; antibody;
ricin-A; cytostatic; catract; lens opecification; epithelial cell;
pBB19; 4137X; monoclonal antibody; MAD; ds.
Synthetic. Location/Qualifiers
cds 1,465

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280 ocgtacacgttcggagggggaccaagctggaaataaaacgggctgaatgctgcaccaact

402

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Query Match Best Local s Matches h 18.6%; Score 81; DB 8; Length 882; Similarity 100.0%; Pred. No. 7.65e-57; 81; Conservative 0; Mismatches 0; Indels 0;

Gaps

S

SULT 11
T70809;
T70809;
T70809;
Source service servery
Nouse anti-idotypic antibody 386 light chain variable region.
Anti-idiotypic; anti-EEPR; epidernal growth actor receptor; tumo;
cancer; neoplasis; glioma; melanoma; carvinoma; drug manufacture;
Mus musculus.
Location/Qualiffiers
cds

signal\_peptide Location/Qualifiers
1.438
/\*tag= a
/note= "no stop codo
1.60
/\*tag= b

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Page 34

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RESULT 14

ID 027340 standard: DNA; 366 BP.

AC 027340 37340; (first entry)

DE 10AN-1993 (first entry)

MR Imminodepressant: organ transplant: av

OS 977549125-A.

PN 0243985-A.
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PH 10-705-1396. 1076-13.
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PH 10-705-1396. 1076-13.
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ID 014651 standard; cDNA; 537 8P.

ID 4-FEB-1992 (first entry)

ID 5-FEB-1992 (first entry)

ID 6-FEB-1992 (first entry)

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Best Local Similarity 100.0%; Pred. No. 6.54-55; 1
Matches 79; Conservative .0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Opery Match 18.2%; Score 79; DB 30; Length 438; Best Local Similarity 100.0%; Pred. No. 6;46-25; Length 438; Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Encodes murine anti-ICAM monoclonal antibody light chain.
Intercellular adhesion molecule; variable region; V(I); mouse;
R6-5-D6 murine WAb; complementarity determining region; CDR; ds.
Mus musculus. Location/Qualifiers
Cds
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14-NOV-1991.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 taracetteggagggggscraagstganatanacgggstgatggtggaccacggta 414
316 TACACGTTCGGAGGGGGACCAAGCTGGANATAANACGGCTGATGCTGCACCAACTGTA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 378 cacgtrogagggggacaagtrggaantaaacgggcgatgstgctgcaccactgatt 437
318 cacgtrogagggggacaagtrggantaaacggcggtgtgtgcaccactgatt 437
318 cacgtrogaaggaggacaagtrggantaaacggcgatgatgctgcaccactgattctgatt 407
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19.75
/*tag= a
19.537
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                                                                                            autoimmune disease;
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RESULT 13
ID 014801 standard; DRA; 537 BP.
AC 014801
DT 13-FEB-1992 (first entry)
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Sequence 537 BP; 135 A;
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27-APR-1990; 08-00958.
27-APR-1990; 08-00958.
(CELL-) CELLTECK LTD.
(ROEM) DOERTHANER MUSILMEIM PHA.
Adair HR. Robinson MK. Bright SM, Rothlein RA;
MPI; 93-33534/48.
P-PSDB; R15199.
Hew humanised chimeric anti-TCAM-1 antibodies - useful in treating inflammation e.g. psorifasis and ulcerative colitis to suppress metastasis of hemantopoletic tumour cell and in suppress metastasis of hemantopoletic tumour cell and in
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318 chccrrccaccaccacchecetgasathanaccgcctgatgetgetgeaccaccaccgate 437
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Κ Op ğ 19 13:23:49 1999

U9-08-836-455-1. rng

pp 11-7M-1992.

pp 27-NOV-1990; 134763.

pp 27-NOV-1990; 197-134763.

pp 27-NOV-1990; 197-134763.

pp 471: 92-78174/34.

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pp 472: 92-

Query Match 17.9%; Best Local Similarity 100.0%; Matches 78; Conservative Score 78; DB 4; I Pred. No. 6.03e-54; O; Mismatches ( Length 366;

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798344 standard; cDN; 380 BP.
798344;
08.ABR-1998 (first entry)
cDN, for y 1,19t chain variable region of anti-asparaginase NAb
Immunoglobulin; ly 1,9ht chain variable region; murine;
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recombinant chimeric polypeptide; ss.

RESULT
AC 199
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US565579 A.

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L1 NOV-1997
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21-MAY-1995
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21-MAY-1995
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Page 3B

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Pf self-protecting chimeric polypeptide comprising biologically active pf adquence of angalanchia antibody sequence. has resistance to e.g. pf disrupting temperatures in antibody sequence. has resistance to e.g. ps Example 2: Columna 7:29 P3 pmc of protecting temperatures (1) Pick Co. The present acquence is the cDNA for the immunopiobulin (2) light CC chain variable region of a mutte anti-apparation of a movel cantibody (PMA). The cDNA was used in the preparation of a movel cantibody (PMA), The cDNA was used in the preparation of a movel comprising a biologically active domain and another domain comprising a biologically active domain and another domain comprising a single chain antibody (SCA) having the light and heavy containing a single chain antibody (SCA) having the light and heavy containing a single chain antibody (SCA) having the light and heavy containing a single chain antibody variable region which specifically binds the containing a single chain specific polypeptide assumes a containing the protection of the containing the cont
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Immunoglobulin; Ig; heavy chain; variable region; murine; human;
recombinant chimeric polypeptide; ss.

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RESULT 19
ID Q46084 standard; cDRA; 739 BP.
AC Q46084,
DT 07-FEB-1994 (first entry)
DE Sequence encoding 52009 sFv protein.
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PD 0.5705.1936.

PD 0.5705.1937.

PD 0.5705.

PD 0.57
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TD 704635 seandard: DNA: 270 BP.
AC 704635; TO 1996 (first entry)
DT 22-MAY-1996 (first entry)
DE Mouse desived light chain RT1 phage antibody pattern A DNA.
NY Light chain: RT2; murine: catalytic antibody: bacteriophage:
OS Mus muscultus.
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PR 21-NUM-1998; US-49826.

PR 21-NUM-1999; US-49826.

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PR 21-NUM-1999; US-49826.

PR 22-NUM-1999; US-49826.

PR 22-NUM-1998; US-4
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Best Local Similarity 98.4%; Pred. No. 1.22e-39;
Matches 123; Conservative 0; Mismatches 2; Indels
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RESULT 20
ID 097504 standard; DNA;
AC Q97504;
PR 409520607-A.

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| 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 161 | 
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PN 21-AN-1395; 001199.
PP 21-AN-1395; 001199.
PP 21-AN-1396; US-187407.
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Sequence 321 BP; 83 A; 79 C; 72 G; 87 T;
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Light chain variable region for monoclonal
Monoclonal mutbody; heavy metal; mercury;
Light chain; ss.
Synthetic.
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285 CA 286
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225 Ttotggtgtcoccamaagsttomgtgcmgtmgtgtcmggtcmgmttattctctccaccat 284
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62; Conservative
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Similarity 100.0%;
62; Conservative
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1..321
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Pred. No. 1.07e-:
0; Mismatches
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Pred. No. 1.07e-38;
0; Mismatches 0; Indels
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1 107e-38; Indels
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variable region
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co by Muly reverse transcriptage, The primers used for cDNA synthesis of the C waps complementary to the 5 and of the CNA synthesis of the C waps domain. Some of the primers used for cDNA synthesis are called the C waps domain. Some of the primers used for cDNA synthesis are converted to the SNA synthesis of the C warrable region of a particular antibody polypeptide was also used for CDNA synthesis are converted to the synthesis of the the synthesi

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Query Match Best Local S Matches 6 n 14.3%; Similarity 100.0%; 62; Conservative Score 62: DB 15; Length 321; Pred. No. 1.07e-38; 0: Mismatches 0: Indels 0;

Gaps

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RESULT RESULT AND RESU

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mat\_peptide Location/Qualifiers 1..446 /\*tag= a

W09622373-A2. 25-UTU-1996: 17-JAN-1996: U00882. 17-JAN-1996: US-372676. 16-JAN-1996: US-372676.

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В 

11-FEB-1993 (first entry)
VL FRPS.
Hidispen: pMELD/1; monoclonal antibody; kappa; light chain; variable region; pWH31; ss.,
Nus macculus.
EP-502812-A.
199-SEP-1992; 810056.
05-FEB-1991; EP-610076.
CCIBA ) CIBA GESTOR AG.

187-54/1.
19.5192.
19.5192.
19.727-JAN-1992.
27.73N-1993.
28. (CIBA) CEBA IEIGY MC.
21. Group: B. Harwerth I, Hynes NE, Nels NS;
27. Zeicki H. (CIBA) CEBA IEIGY MC.
21. Zeicki H. (CIBA) CEBA IEIGY MC.
21. Zeicki H. (CIBA) CEBA IEIGY MC.
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Query Match 13.1%; Best Local Similarity 98.9%; Matches 87; Conservative Score 57: DB 8: Length 1605; Pred. No. 5.14e-34; O: Mismatches 1: Indels 0; Gaps

1276 atcoagstaccoagsciccatcocottatctgcotctotgggagaaagagtcagtctc 1335

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SULT 25 028254 standard; DNA; 407 BP 028254; 11:FEB-1993 (first entry) VL\_FRP5. 407 BP.

RESULT RE

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pWR11 which was used in the construction of a recombinant antibody which is directed to the extracellular domain of the growth factor c-extbs-2.
Sequence 407 BP; 101 A; 107 C; 94 G; 105 T;

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Query Match Best Local S Matches 5 h 12.9% Score 56; DB 4; Length 407; Similarity 100.0%; Pred. No. 4.37e-33; S6; Conservative 0; Mismatches 0; Indels 0; Gaps

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339 tgaantaansggetgatgetgatocaactgtatocatetteceaccatocagt 394

mat\_peptide signal\_peptide

Proceedings of the producting anti-tobacco mosaic virus antibody - Press; Reference 1-14; Tesperior of the total control of total control o

Length 961;

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Query Match 13.1%; Best Local Similarity 100.0%; Matches 57; Conservative Score 57; DB 25; Length 447; Pred. No. 5.14e-34; 0; Mismatches 0; Indels 0; Indels 0; 447 0

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DE SE SE SY
PH NEED NO. SULT 24.

SULT 24.

04608 standard; cDNA; 1605 BP.

04608 standard; cDNA; 1605 BP.

04608 c standard; cPIT;

Sequence encoding G-PIT;

Sequence antigen; c-erbB-2; G-PIT; ss.

1 mout antigen; c-erbB-2; G-PIT; ss.

prythetic: Location/Qualifiers

1,11605

cds 1,11605 Ş B

Location/Qualifiers 1..1605 /\*tag= a

W09316185-A. 19-AUG-1993: U01055

US-08-836-455-1.rng

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Jocation/Qualifiers
34..753
/\*tage A
94..93
/\*tage b
94..750
/\*tage c

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st Local Similarity 100.0%; Pred. No. 4.37e-33; tches 56; Conservative 0; Mismatches 0;
US-08-836-455-1.rng
                                     Indels
                                   0
                                     Caps
                                     0
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054651; 994 (first entry)
784.12 light chain.
784.12 light chain.
Chimerio: carcinoembryonic antigen; CCA; murine; mouse; constant; region; transform; myeloma cell; light chain; tumour; ss.
Synthetic Location/Qualifiers
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14..950

/rtag= a /product= T84.12\_light\_chain

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I Flacher R. Parton ...
I Republic Research ...
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23-DEC-1993.
15-TUR-1993; U05709.
15-TUR-1992; U5-904074.
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(YARC) YANG T.
Pischer R. Paxton R. Sh

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Score 56; DB 9; Length 1041; Pred. No. 4.37e-33; 0; Mismatches 0; Indels 0;

h 12.9%; Score 56; DB 9; Length 1041; Similarity 100.0%; Pred. No. 4.37e-33; S6; Conservative 0; Mismatches 0; Indels 0; 462 0

RESULT 19
ID 090430: Quantum de la company d

clone chain;

3KB11. immunoglobulin;

Location/Qualifiers
1..354
/\*tag= a
/product= anti-autoantibody\_Idio3

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RESULT 28 ID Q54651 standard; CDNA: 1041

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pp M 07701999-A.

PP 18-APR-1991 272950.

PF 08-CCT-1991 7P-27250.

PR (ACAC) HACTMARA T.

PR 08-CCT-1991 TP-27250.

PR 19-BSB: R74965.

PR 19-BSB: R74966.

PR 19-BSB: R74966.
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g Overy Match 21.4%; Score 54; DB 16; Length 354; Best Local Similarity 100 0%; Pred, No. 312e-31; Matches 54; Conservative 0; Hismatches 0; Indels 0; 301 tanongitteggaggggggechaggtsganatanancgggtggtggtggtgcaga 334
316 TACACGTTCGGAGGGGGACCAAGCTGGAAATAAAACGGCTGATGCTGCACCA 399

0

770811 standard: DNA: 429 BP.
770812 standard: DNA: 429 BP.
770813 standard: DNA: 429 BP.
770814 standard: DNA: 429 BP.
770815 standard: DNA: 429 BP.
770817 primer\_bind signal\_peptide Location/Qualifiers
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Location/Qualifiers
Location/Qualifiers codon given" . . ..

EP-745612-A1.
04-DEC-1996.
14-MAY-1996; 107651.
126-MAY-1995; EP-107967.
126-MAY-1995; EP-107967.
126-MAY-1995; AP-107968.
126-MAY-1995; AP-107968.

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Rosell E;

primer\_bind

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P-PSDB; N19580.

Monoclonal anti-idiotypic antibodies mimicking epidermal growth factor receptor useful for tumour therapy (1416). The receptor useful for tumour therapy (1416). The receptor (1586) app. English: antibodies, 1588, 386 and 586 are new. They induce an immune response against epidermal growth factor receptor (1587). The sequences of the heavy and light chain variable regions of these antibodies are given in the specification. The antibodies are used for the manufacture of drugs directed against tumours that express BGFR on their surface, including melanomas, glamms and carcinomas, glamms and carcinomas, glamms and carcinomas, also make the special sequence (1588). 109 N; 104 C; 100 G; 116 T;

Query Match 12.4%; Best Local Similarity 100.0%; Matches 54; Conservative Score 54; DB 30; Length 429; Pred. No. 3.12e-31; 0; Mismatches 0; Indels 0; Gaps

0

170807 standard: DBN, 441 br.
10048 anti-idiotypic anti-body 1588 light chain variable region.
10048 anti-idiotypic anti-body standard growth factor receptor; tumour.
10104 cancer: neopicals glions; malanoma; carcinoma; drug manufaccure; as.
10104 cancer: neopicals; glions; malanoma; carcinoma; drug manufaccure; as.
10104 cancer: neopicals; glions; malanoma; carcinoma; drug manufaccure; as.

primer\_bind primer\_bind signal\_peptide 1.441
/noge no stop codon given
ie 1.72
b 1.72
/tug b 1.434
/tug d 1.434
/tug d 4.6.8441

gp-745612-A1

G-DEC-1996

14-MAY-1999; 107651

26-MAY-1999; ED-107967

MERE ) MERCH PATENT OMBE

Adan J Carceller A Gomes A, 1

PF189 9-013583/03
PF189 18976; Granti-idiotypic antibodi
Monoclonal anti-idiotypic antibodi Piulata J, Rosell

growth

Wonoclonal anti-idiotypic antibodies mimicking epidermal factor receptor - useful for tumour therapy Claim 6: Fig 58: 28pp: English.

Page 50

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US-08-836-455-1.rng

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Page Mon Apr 19 13:23:49 1999

Length 751;

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Gaps

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RESULT 14

TO CHOOSE standard; cDNA; 2001 BP.

A C 46088 34 atandard; cDNA; 2001 BP.

A C 46088 34 (first entry)
D1 97-FEB-1994 (first entry)
D2 sequence smooding 741 sFV-FE40.

EN Single chain FV polypeptide; yW-VL het
EN Single chain FV polypeptide; yW-VL het
EN Single chain FV polypeptide
EN Single chain FV polypeptide
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PT New single chain FV polypeptide bindin
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Produced the control of the 
                19-7NN-1997, 11-7NN-1995, 007-507, 19-7NN-1995, 007-507, 19-90534, 01-7NR-1994; 005-206190, 01-7NR-1994; 005-206190, (SMIX) SMITMALINE BECHAN CORP. (SMIX) SMITMALINE MR. Jackson JR. Young PR.
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751437 standard; DNA; 751 BP.
751437 standard; DNA; 751 BP.
751437 standard; DNA; 751 BP.
751437 standard; Clist entry)
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They induce an immune response against epidermal growth factor receptor (SCFR): The sequences of the heavy and light chain warlable regions of these antibodies are given in the specification. The antibodies are used for the manufacture of drugs directed against unbours that express SCFR on their surface, including melanomas, globmas and carcinomas.

Sequence 441 BP: 111 A; 110 C; 104 G; 116 T;
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371 TGGANATAMACGGGCTGATGCTGCACCACCACTGTATCCATCTTCCACCATCA 424
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Similarity 98.8%;
82; Conservative
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ed monoclonal antibodies with donor :
p. against CD38, useful for treating
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No. 3.12e-31; 54; Conservative 0; Mismatches 0;
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Pred. No. 2.17e-29;
O: Mismatches 1: Indels
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TO 31-34.1907 (first entry)
DE Humanised anti-CD18 mono-Conal antibody variable light chain.
RY HOTO-CLORAL antibody; Mab. humanised; cancer. auto-Lughe disease;
RY HOTO-CLORAL antibody; Mab. humanised; cancer. auto-Lughe disease;
RY multiple myeloma; lymphoma; rheumatoid arthitis; CD18; disease;
RY complementary determining region; CDR; heavy chain; light chain; ds.
RY complementary determining region; CDR; heavy chain; light chain; ds.
RY complementary determining region; CDR; heavy chain; light chain; ds.
RY complementary determining region; CDR; heavy chain; light chain; ds.
RY complementary determining region; CDR; heavy chain; light chain; ds.
RY complementary determining region; CDR; heavy chain; light chain; ds.
RY complementary determining region; CDR; heavy chain; light chain; ds.
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Promoting large a 71-74; 87pp; English:

Contample; pages 71-74; 87pp; 87p
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PRECOMMINANT and humanised chimeric antibodies against human PT interleukin-beta for preventing and treating T interleukin-beta for preventing and treating T interleukin-mediated inflammatory disorders that S (Laim 21, Page 36-39, Sapp. English.

Colonated nucleic acid sequences (T31436 and T31437) respectively controlled to the heavy chain (W11919) of 1314 chain (W11918) of C anti-human interleukin-1 beta (III-1 beta) murine monoclosal (C anti-human interleukin-1 beta (III-1 beta) murine monoclosal controlled to the season of the many controlled for the many can be a few of the many can be a few of the many can disher the season with the season colon of the many can be a few of the complete can be season calls of the prevention of III-1 mediated inflammatory disorders until and sequence (T31 BF) 212 A; 186 C; 180 G; 173 T;
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Best Local Similarity 100.0%;
Matches 51; Conservative
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Best Local Similarity 98.8%;
Matches 84; Conservative
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10234 standard: DBA; 391 BP.
1003224 standard: DBA; 39
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10566070-A.

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Best Local Similarity 100.0%;
Matches 48; Conservative
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Best Local Similarity 100.0%;
Matches 48; Conservative
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Example F: P19 24; 114pp; English

A cDNA insert (70378) in vector penishent region of anti-rabbit

chain variable region and part of the constant region of anti-rabbit

interleution of count deart of the constant region of anti-rabbit

by amplification of cDNA derived iron 64: 2 5 producing hybridosa cells

using primers (70371; 74) based on light chain sequences. It is

used with cDNA (70379; ooding for the heavy chain variable region

in the produced anti-IL-8 mouse-human chineric Pab.

sequence 391 BP; 95 A; 105 C; 94 G; 97 T;
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VIOIO (100 tandard; DNA; 391 BP.
VIOIO)
O-UNN-1998 (first entry)
O-UNN-1998 (first entry)
O-UNN-1998 (first entry)
Light chain variable region DNA.
Monoclonal antibody; Mab 664.2.5; interleubin-8; II-8; murine;
Light colitie; immunotherapy; bacterial pneumonia; variable region;
Creatment; light chain, heavy chain; neutrophil chemotaxia inhibitor; sa.
Nus ap.
Location/Qualiffice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Decrachuk CM. Fong S. Herbert CA. Kim KJ. Leong SR:
WFI: 99-30580/ 1997.
P-PSUB: 886321.
Inflammatory disorders, partic ulcerative colitis, and bacterial
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Pred. No. 9.84e-26;
0: Mismatches 0;
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Pred. No. 9.84e-25;
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Length 391; Indels 426

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T03378; standard; cDNA; 391 BP.
T03378; 996 (first entry)
Anti-TL-8 MAD 664.2.5 light chain variable region cDNA.
Anti-TL-8 MAD 664.2.5 light; chain variable region LDNA.
Monoclonal antibody 664.2.5; MAD; interleukin-6; IL-6;
chimeric antibody; Fab; antibody engiaering; inflammation;
inflammatory bowel disease; ulcerative colitis; bacterial p
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G. G. Mos701354-Al.

PM Mos701354-Al.

PD 16-JMN-1997. 110.03.

PR 27-JWN-1995. US-49.314.

PR 27-JWN-1995. US-49.314.

PR 27-JWN-1995. US-49.314.

PR 16-BERT CA. Ababaseff RC. Moore MM:

PR 17-SPEDE MAJNE.

PP 7-SPEDE MAJNE.

PP Treating asthma by admin. of interleukin-8 anta-

PP antibody that inhibits shinding of IL-8 to neutral chemotasis and elastase release example G: PNg 24; 101pp; English.
                                                                                                                                                                                                                                        IIT 38
778588 standard; cDNA; 391.8P.
778588; (first entry).
NONCOLONAL ARIBODAY 664, 2.5 variable light chain region encoding cDNA.
NONCOLONAL ARIBODAY 664, 2.5 variable light chain region encoding cDNA.
Interrebikin-8; II-8; antagonias; anti-interrebikin-8 antibody; asthma;
inflammatory disorder; neutrophil reportatis; releases; rel
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Score 48; DB 38; Length 391 Pred. No. 9.84e-26; 0; Mismatches 0; Indels

Length 391;

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Pr and/or heavy chain equences; used to prevent interleukin-8 mediated Pr neutrophil observate. Programme of the process of the constant region of the nurine monoclonal antibody 561.25. This cDNA constant region of the nurine monoclonal antibody 561.25. This used in the vector primarb to constant programme of a chimeric 664.25. Fab weator by various recombinant creimiques. This chimeric 664.25. Fab weator by various recombinant constant region of a chimeric fab complementarity determining the chimeric fab complementarity determining the constant region of a light chain and/or a heavy chain variable region from the new constant programme obtained the constant region of the new constant programme obtained the constant region of the human immunociphila programme obtained the constant region of the human immunociphila from the constant which is used to be treat the collisis and bacterial paramonia.
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Best Local Similarity 100.0%;
Matches 48; Conservative
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Nev recombinant DNA encoding chimeric antibody - with human constant and non-human variable regions, esp. directed spainst interleukin 2 receptor rec
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Similarity 100.0%; Pred. No. 9.84e-26;
48; Conservative 0; Mismatches 0;
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                                                                                                                                                                        immunosuppressant - and monoclonal anti-IL2R
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                                    RESULT.

1 DO O.55115, standard; DNA; 435 BP.

AD O.55115, standard; DNA; 435 BP.

DZ 16-MAR-1997 (first entry)
PZ 05-MAR-1997 (first entry)
PZ 16-MAR-1997 (firs
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DE ULTS: 41

DE ULTS: 41

DE ULTS: Chimeric antibody light chain clo

RM Interiekthor3: immunosuppressant.

OS Chimeric Raco asplens

Fir cds

Fir cds

Fir ds

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Fir signal_peptide 1.60

Fir mat_peptide 5.42

Fir mat_peptide 5.42

Fir mat_peptide 61.432

Fir mat_peptide 5.42

Fir mat_peptide 61.432

Fir mat
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B PPE: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 13:23:49
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48; Conservative 0; Mismatches 0;
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Query Match Best Local & Matches

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N91663 standard: DNA:
27 14-NR-1990 (first entry)
DE Light chain of monoclonal antibody 6A4.
RH Monoclonal antibody 6A4; light chain: Pseudomonas aer
FH Key
cds /\*tag\* a
/\*tag\* a The hallow region of the probability of the hallow region was a possible of the probability of the probabili Query Match
11.0% (Score 48; DB 1;
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19-JAN-1999. 299617.
19-JAN-1999. 05-903971.
02-SEP-1996. 05-903971.
19-JAN-1999. 05-999617.
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19-80-200390.3 Key Location/Qualifiers Location/Qualifiers 127 47

G65811 standard; CDNA to mRNA; 612 BP.

G65811 standard; CDNA to mRNA; 612 BP.

G125NA-1995 (first entry);

Porphyrin antibody light chain coding sequence.

Light: heavy: chain; monocidal antibody; porphyrin;

Light: heavy: chain; monocidal activity; ds.

Mus musculus.

Location/dualifiers rat antibodies. The DNA sequence provides much higher yields of chimeric antibodies than known methods. See also 015114-015118. Sequence 435 BP; 107 A; 130 C; 101 G; 107 T; 07-JAN-1991 (first entry)
Light chain of anti-bovine growth hormone MAB.
Monoclonal antibody: ss. standard; DNA; 489 h 11.0%; Score 48; DB 3; Length 435; Similarity 100.0%; "Pred. No. 9.84e-26; "Victoria 48; Conservative 0; Mismatches 0; Indels eptide chain binding molecules - having light chain ion of antibody linked by peptide to heavy chain ion US-08-836-455-1.xmg 0; Indels Length 588; Length 435; aeruginosa; 0; 0 1-460 Gaps Caps .. 0 Page Mon RESULT AC TO AC TO DE OS RW EA OS MU EA OS MU EA PT CA PT CA PT CA PT CA PT TO PT RESULT 46 ID Q05709 4 AC Q05709; 5 B 5 B Windows (1982).

Proceedings: Use (1982).

Processing in Use (1982).

Proce Fig. J06105666.A. from the Specification Fig. J06105666.A. from the Specification Fig. J07105666.A. Fig. J07105666.A. J07105666.A. J07105666.A. J0710566.A. J07105 ğ Query Match 110%; Score 48; DB 11; Length 612; Best Local Similarity 100 0%; Pred, No. 9 84e-26; Matches 48; Conservative 0; Mismatches 0; Indels Query Match 11.0%; Score 48; DB 2; Length 489; Best Local Similarity 100.0%; pred. No. 9 846-26; Matches 48; Conservative 0; Hismatches 0; Indels W09629426-A1. 26-SEP-1996. 17-MAR-1995; J00462. 17-MAR-1995; WO-J00462. (PROT-) PROTEIN ENG RES I T97816 standard; DNA; 646 BP.
T97816;
T97816;
09-DEC-1997 (first entry)
09-DEC-1997 (first entry)
catalytic antibody; enantioselective hydrolysis;
EA/7612; EAA/362; de. 19 14-UDN-1991 (first entry)
Encodes murine monoclonal 14.18 i chain V region.
Chimaeric hinding protein; immunoglobulin; variable
light chain, as
Hus musculus. mat\_peptide 433 lamegggctgatgctgcaccaactgtatocatcttcccaccatccagt 480
379 AAACGGCTAATGCTGCACCAACTGTATCATCTTCCACCTTCCACGT 426 ignal\_peptide 13:23:49 standard; 1999 Location/Qualifiers
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RESULT 45 ID Q11292 AC Q11292;

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Come patent discloses new natural presents which hydrolyse amino condessers enantioselectively prefeably as exters at the factor of the hydrolyse amino acid exters enantioselectively prefeably as exters are the hydrolyse amino acid are extensed to the enteritted amino acid are supposed the presents of the catalytic condessers of the hydrolyse prefeably and shadoly press specially shafoly (FERN SP-4947) and shadoly (FERN SP-4947) and s
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DOL335 standard; DNA: 648 BP.
DOL335; standard; DNA: 6
                                                                                                                                                                                                                                                                                                                                                                                      to engineer, more stable and less expensive Example 1: Fig 22: 78pp; English.

CDM, clones 1793056 and 720507) respectively code for the heavy. CDM, clones 1793056 and 720507) respectively code for the entry-chain (872776) and light chain (872777) of the entri-bowine growth monoclonal antibody 302, an 1961 antibody with a gamma 1 heavy chain and kappa light chain. Sequences encoding the heavy and light chain can be incorporated into novel constructs as the construct of the cons
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Sequence 646 BP: 182 A; 174 C; 152 G; 118 T;
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Sequence encoding mouse anti-bovine growth hormone MAb light chain.
Monoclonal antibody; MAb; affinity; binding; antigen; diagnostics;
therapy; langing; purification; blosensors; as.
Mus musculus.
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WPI: 96-443199/44.
P-PSDB; W15933
Catalytic antibody for enantiosel:
cesters - also new hybridoma secre
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Similarity 100.0%;
48; Conservative
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Pred. No. 9.84e-26;
0; Mismatches 0
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28 279057;
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GB_RO: MMUGB675
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GenBank, Release 110.0, Released on 14Dec1998, Formatted on 15Dec1998
EMBL, Release 56.0, Released on 16Sep1998, Formatted on 15Dec1998

word-size: 15 Words: 182747 Diagonals: 6,088 Total diagonals: 2,000,000,000
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foon, kenneth a.
chatterjee, sunil k. .
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X02177 M.musculus mRNA for IgK kappa
U30236 Mus musculus anti-DNA antibody
U88676 Mus musculus anti-DNA antibody
Z22118 M.domesticus IgK variable regi
M12191 Mouse Ig active kappa-chain vJ
X82890 M.musculus IgGl, light chain v
U25098 Mus musculus anti-Pseudomonas
S69053 Ig V kappa -anti-Pnitrophenyl
AF003294 Mus musculus Ig kappa light
X02178 M.musculus mRNA for IgG kappa
U62776 M.musculus mRNA for IgG kappa
                                                                                       AF003291 Mus musculus IgG kappa light AF003299 Mus musculus IgG kappa light U21066 Mus musculus Immunoglobulin ka AF023475 Mus musculus anti-pneumolysi K00880 mouse ig kappa germline v geng 100568 mouse ig kappa unproductively v00760 Mouse pseudogene for kappa-imm AB016620 Mus musculus mRNA for Immnog X03382 Mouse mRNA for GAT (HP27) anti X900300 Musmusculus antibody light chai AF003300 Mus musculus IgG kappa light S5170 nitrophenyl phosphonate-specif U1937 Mus musculus immunoglobulin ka
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X03383 Mouse mRNA for GAT (HP22)
X03384 Mouse mRNA for GAT (HP29)
U19326 Mus musculus immunoglobul:
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SUMMARIES

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Title:
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>US-08-836-455-1 (1-435) from US08836455.seq 435

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Scoring table:

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Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U. Distribution rights by Oxford Molecular Ltd

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### System	Non Apr 19 13:23:48 1999 US-08-836-455-1.xge	### MINISTERS   MANISTERS	Mon Apr 19 13:23:48 1999 Us-08-835-455-1.rge
	Page 19		Page 17
### STATEMENT OF THE PROPERTY	Mon Apr 19 13:23:48 1999 US-08-836-455-1.rgs	### 1.00	Man Apr 19 13:23:48 1999 US-08-836-455-1.rge

27 6.2 1598 32 582493	27 6.2 1181 26 HSIGK3	26 HUMIGKVV	27 6.2 945 22 A21386	27 6.2 920 22 A62068	27 6.2 824 32 SYNMA15C5	27 6.2 800 26 HUMIGKVB	27 6.2 798 32 AF000955	27 6.2 797 22 A56709	27 6.2 732 22 813410	27 6.2 711 32 SYNIGLO	27 6.2 464 22 125724	27 6.2 464 22 A29573	27 6.2 439 26 HSU43764	27 6.2 432 29 MMU27013	27 6.2 424 26 HSIGKLCH	27 6.2 389 26 HSIGNIV21	27 6.2 387 26 HUMIGK	27 6.2 385 28 HSTGKL12A	27 6.2 385 20 MMARBTONT	27 6.2 382 29 MMCBAIGKL	27 6.2 382 29 MMSJIGCKL	27 6.2 381 26 HS3D6LCV	27 6.2 376 26 HSIGKLV22	27 6.2 369 28 HSKPOLC20	27 6.2 369 22 187032	27 6 3 360 20 HSLGALVAU	6.2 363 29 MUSIGRAPB	27 6.2 360 29 MUSIGLOH	27 6.2 360 29 MUSIGLES	27 6.2 360 29 MUSIGKAF	27 6.2 360 29 MUSIGD 1	-	Mon Apr 19 13:23:48 1999
14-IFN- tau =fusion ge 3.82e-07		Sequence 4 irom Patent 3.82e-07					Mus musculus single ch 3,82e-07	from Paten 3.82e-07		Synthetic Is light the 3 BJ#-O/	Sequence 15 from paten 3.82e-07		_			H. sapiens mrnh for rea 3.82e-07	Human II rearranged &s 3 82+07	CONTRACT AND CONTR	Oglobulin 1 3.82e-07	(CBA) IS ka 3.82e-07	M.musculus (SJL) Ig ka 3.82e-07	for 3D6 lig 3.82e-07			Sequence 19 from paren 3.02e-07		_		Mouse rearranged light 3.82e-07		dus musculus immunoglo 3.82e-07	•	US-08-836-455-1.rge Page 21
	BASE COUNT 78 A 71 C 70 G 91 + 1 C+5	/translation="SPSSISASIGERVSLICERASQDIGSSLAWIQQEPDGTIRRLIYA	/db_xref-"PID:q197632"	/product="immunoglobulin kappa-chain VX-1"	/codon start	(TON (T		gene 1303	/map="chromosome 6"	/tissue_type="hybridoma"	/cell_line="H220-23"	/db krafe*texon:10090*	/actain anda/c	CHANTEN SUS MUSCULUS		reatures Location/Qualities	by J. Kava	In press   kindly submitted		MEDLINE 90375932	JOURNAL J. Immunol, 145, 2312-2321 (1990)	hemacrittish			REFERENCE 1 (bases 1 to 303)	Murinae: Mus.	Vertebrata; Eutheria; Rodentia; Sciuroquathi; Myomorpha; Muridae;	:	ORGANISM Mis miscillia		processed gene.		Mon Apr 19 13:23:48 1999

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RESULT 1
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DEFINITION
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Ruman Kappa immunoglob 3.82e-07
Artificial sequences f 3.82e-07
Artificial sequence ex 3.82e-07
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Best Local Similarity 98.6%;
Matches 216; Conservative
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Pred. No. 1.97e-152:
0: Mismatches 3: Indels 0:
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MUSIKCC 390 bp mRNA, ROD 24-7UL-1997

DEFINITION Mis musculus immunoglobulin kappa chain mRNA, 5' end of cds.

MCCESSIOS 9198110

ETHYRORDS immunoglobulin kappa chain.

SOURCE Mission of the control of the 
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Leakurs, K.

Lieert Submission

Mindertted (24-07U-1997) Immunology, Mayo Clinic, 200 First Street

W. Bochester, May 5595, USA

W. Bochester, May 5595, USA

Location/Qualifiers

1. 399
                                                                                                                                         /organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
/db_xref="taxon:10000"
/cell_line="hybridoma_HNK-l"
/coden_start=1
/product="immunoglobulin kappa chain"
                                                                                         >390
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ACCESSION US>>-,
NID
GIB70231

EXPRODES
SOURCE

ONCANISH Hus musculus
ONCANISH Elikaryotes; intochondrial sukaryotes; Metasoa; Chr
Vertebrata; Entheria, Rodentia; Solurognathi; Mur
vis. --1 to 302)
"-T. and Marion,T.N.
derived VH-CDR3

; Chordata; Muridae; Murinae;

JOURNAL REFERENCE AUTHORS TITLE JOURNAL

Tibhases 1 to 302)

Krishnan, H., Jou.N.-T. and Marion, T. N.

Correlation between sometically desired VM-CDB3 structures and specificity for DNA among autoimmune antibodies to DNA

J. Immunol. (1997) in press

(hazes 1 to 302)

Marion, T. R.

Ma

DASE COUNT ORIGIN

>31. >302
/codon\_start1
/product\*\*anti-10N immunoglobulin light chain IgG\*
/broduct\*\*anti-10N immunoglobulin light chain IgG\*
/branalation\*\*MTMSPSSLSAS/LERVISTRASODIOSSLAWIGOEBDGTIKEL
IVATSLLDGUPKESGSRGSDTSLIISSLESDPVDVCLQYASSPTFCGGTKL\*
74 a 72 c 71 g 84 t 1 others

/organiam="Mus musculus"
/strain="(NED x NEW) F1"
/force="mouse number 363"
/foth\_tref="taxon:10090"
/cell\_tine="363.62"
/cell\_type="hybridoma"
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<l...>302
<l...>302

Guery Match 31.8%; Score 147; DB 29; Length 302; Best Local Similarity 99 0%; Pred No. 1.17e-141; Matches 207; Conservative 0; Mismatches 2; Indels 0;

Gaps

RESULT 2
LOCUS
DEFINITION

MON55589 102 bp mRRA ROD 05-MAR-1997 Mus musculus anti-DDA immunoglobulin light chain IgG, antibody 1518-62, partial cds. US558-62, partial cds.

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283 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCT 342

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Mon Apr 19 13:23:48 1999

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Page 26
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COMMONT.K.C., FAITELLY, P., HORIKAWA, A. and Stollar, B.D.

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COMMONT.K.C., FAITELLY, P., HORIKAWA, A. and Stollar, B.D.

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O'COMMONT.K.C., FAITELLY, P., HORIKAWA, A. and Stollar, B.D.

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343 CCGT 346
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2 1 (bases 1 to 324)

AS Moore, K. N. and Exidatoni.A. composition

AND Patent: US 462334-4 4 10-FEB-1887;

DNAX Research Institute of Molecular and Cellular Biology, Inc.

Location/Qualifiers

1. .324 "mm"unknown" 87 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARO45508 381 bp. mRNM.
No masculus doll enti-poly(dC; monoclonal antibody kappa light
chain variable region, (ign) mRNM, partial cds.
ARO45508
g2906099 | | |
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Sequence 4 from Patent US 4642334.
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/product="immunoglobulin kappa chain"
96 a 90 c 95 g 109 t
                                                                                                                                                                                                                                                 Organism="this musculus"

**Etails="CJTML"

**Charter="this musculus"

Celliline="gleen cell hybridoma"

Chromosoms="6"

Clone="CCO"

41..>381

Jenn="ign"

1..>81

1..>81

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1..>81
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/translation**MONHAPAGIFGFILLLEFOGTRCDIQHTGSP8SLSASIGERVSLT
CRASCOLGSLEMTLOGEROTIKHLIKAYSSLDSGVPKRFSGSRSGSDTSLTISSLES
EDFVDYCLGVASSFYFTGGGTKLEIKR*
1. 390
61. >>390
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chain
/braduct="anti-poly(dC) monoclonal antibody kappa light
chain
/bb_ref="piD:92906100"
/bb_ref="piD:92906100"
/bb_ref="piD:92906100"
/cranalation="MRAPAQIFOFILILIFPGTRCDIQMTQSPSSISASIGERVSLTCR
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     ACCESSION PRETY COM-
REPRONDS
SOURCE
ORGANISH Mus musculus
Vertebrate, Namaalia, Eutheria; Rodentia; Sciurognathi; Muridae;
Murinos; Mus.
1 (Dases 1 to 443)
AUTHORS
Shilts, L.D.
Yable mochesten anti-DNA antibody
Westhoff, C.H., Wylle, D.E., Kathol, S., Whittier, A., McHugh, J. and
AUTHORS
Shilts, L.D.
Yable mochesten anti-DNA antibody
Westhoff, C.H., Wylle, D.E., Kathol, S., Whittier, A., McHugh, J. and
AUTHORS
Shilts, L.D.
REPERENCE
Heathoff, C.H., Wylle, D.E., Kathol, S., Whittier, A., McHugh, J. and
AUTHORS
Shilts, L., Mylle, D.E., Kathol, S., Whittier, A., McHugh, J. and
AUTHORS
Shilts, L., Wylle, D.E., Kathol, S., Whittier, A., McHugh, J. and
AUTHORS
Shilts, L., Wylle, D.E., Kathol, S., Whittier, A., McHugh, J. and
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7

LOCUS MORBESTS 443 bp mRNA ROD 02-MAY-1997

DEFINITION Hus musculus anti-DNA antibody light chain variable region mRNA,

ACCESSION 08675 de.

ACCESSION 08676 DE COMMANDE COM
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FEATURES
Source
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AUTHORS HOUSE K. H. and Kaffaroni.A.
TITLE Hybrid DNN, binding composition prepared thereby and therefor JORRAND Patent: EP 0088994-A2 4 21-8EP-1981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5

LOCUS 17835 224 bp

DEFINITION Sequence 4 from Fatent EP 0088994.

ACCESSION 958947

RID 988947

REPWORDS Unknown.

ORGANISH Unclassified.
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Best Local Similarity 99.9%; Pred No. 6 Ole-112; Length 381;
Matches 192; Conservative 0; Minmatches 2; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 28.0%;
Best Local Similarity 98.9%;
Matches 182; Conservative
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Best Local Similarity 98.9%; Pred. No. 6.0He-112; Indels 0; Gaps
Matches 182; Conservative 0; Mismatches 2; Indels 0; Gaps
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1111
343 CCGT 346
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343 CCGT 346
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223 GGTCTGGTCCCCANANGGTCGGTCGGTCAGATAGGTCTGGTCAGATTATTCTCTCACC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 TOCCTTCACCAGAACCAGTGAACTATTMAACCCTGATCTACCCCACTTCCACTTTA 272
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283 ARGACCAGCCTGAGTCTGAAGATTTTGTAGCCTATTACTGTCTAGATTATGTAGTCT 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 ANTERROPERCENAAGETENGERGEAGTAGGETEGGETENGATTANTERTERGAGE 222
223 GETTETGGTGCCCANAAGETENGTGCCAGTAGGTCTGGGTCNGATTATTETCTCAGE 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 TOGETTCACCAGANCCAGTCGANCTATTALACGCCTCATCTACCACCACATCCACTTTA 162
163 TGGCTTCAGCAGANCCAGTCGANCTATTALACGCCTCATCTACGCCACATCCACTTTA 222
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Location/qualifiers
1. 324
/organism="unknovn"
82 a 80 c 75 g 87 t
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Pred. No. 6.01e-112;
0; Mismatches 2; Indels 0;
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processes

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RESULT 9
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
SOURCE
ORGANISM
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NID
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LOCUS VALUES 19 kappa active gene: V441 VJ region.
ACCESSION 400858 19 kappa active gene: V441 VJ region.
ACCESSION 4008531 V region: V-region; complementarit
EXTMORDS C region; J region: V-region; complementarit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
Source
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Best Local Similarity 98.9%;
Matches 182; Conservative
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343 CCGT 346
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233 GGTTCTGGTGTCCCAMAGGTCAGTGCACTAGTGTCAGCTAACTATTCCCTCACE 282
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|||||
343 CCGT 346
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283 ARRACKACCTTCAGCTTCAAGAITTINGTAGACTAATTACTGTCTAGAATANTCTAGTCT 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           differentiated gene; Ig kappa light chain; immunoglobulin. Num unoglobulin Num unoculum Bukaryotae; mitochondrial
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//gene='lgk'
/
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                                                                                                                                                                                        Muriner, Mus.

1 (base 1 to 685)

2 (base 1 to 685)

3 (setdman,)-G., Max.E.E. and Leder,P.

4 kapps immunojaboliin gene is formed by site-specific second instance without further somatic mutation second instance without further somatic mutation page 10 (572)

7821)100,000 (572). 370-375 (1979)
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framework region; hypervariable region; immunoglobulin light chin;
immunoglobulin-kappa; immunoglobulin-kappa sibgroup vk-5; processed
                                                                                 MMU.IGRAP.MOPC41.
Location/Qualifiers
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108 a 109 c 113 g 113 t
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brata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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KEYWORDS

KEYWORDS

house mouse.

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ORGANISH Mas muscults

Entharyotes: mitochondrial sukaryotes: Metazoa; Chordata;

Terebreta; Entheria, Rodentia; Sciurognathi; Myomorpha; Muridae;

Murinae; Mus has 1 to 273)

AUTHORS

Reperance 1 (bases 1 to 273)

AUTHORS

Reark, J. M., Kunts, C.L., Nguyen, K.A., Mandik, L., Cattermole, M. and

AUTHORS

Reperance 1 (bases 1 to 273)

Reark, J. M., Kunts, C.L., Nguyen, K.A., Mandik, L., Cattermole, M. and
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It is a productively rearranged kappa ig from myeloma mopod, the tentes as a productively rearranged kappa ig from myeloma mopod, the tentes betted in the situes belte refer to the published differences mother than and active genes, they are probably typographical errors that the committee and active genes, they mutation has occurred after recombilated [1] says that no somatic communication) as id that the published on myells are stance is correct region exon results in a lowered rate of transcription somether than a course of the site of transcription initiation, the deletion moves transcription initiation coden to about 20 ps 5 cor part of the vidi content gene and part of the vid content segmentary. For the germine joining it region see unsighed to respectively for the germine joining it region are unsightly and the gene table table cdr-complementarity determining region and frefitments testing the cdr-complementarity determining region and
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Seddman, J.G., Max. E. and Leder, P.
A kappa Liminoglobulin gene is formed by site-specific Recombination without further somatic mutation dature 200 (5721), 370-375 (1979)
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brata; Eutheria; Rodentia; Sciurognathi; Mycmorpha; Muridae;
ae; Mus.
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DPTOTTCQTASSPMTPGGCTKLEIKR*
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Pred. No. 6.01e-112;
0; Mismatches 2; Indels 0; Gaps
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US-08-836-455-1.rge

ROD 14-FEB-1996 V-J regions mRNA, clone

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Mon Apr 19 13:23:48 1999
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in MRL-lpr/lpr mice J. Immunol. 154 (9), 4444-4455 (1995)

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US-08-836-455-1.rge

Page 33

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US-08-836-455-1.rge

Page 34

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Ouery Match 27.6; Score 120; DB 29; Length 273;
Best Local Schilarity 93,1; Pzed No. 1.18-109; Length 273;
Matches 150; Conservative 0; Minatches 1; Indels 0; Gaps 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 ANTENGENENCCIAAAAGETRAGTEGAGTRAGTENGGTCAGATTATTCTCTCACC 185
213 GETTCTGGTCTCCCAAAAGETRAGTCAGTCAGTAGATTATTCTCTCACC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MENYEMBELI 279 bp. RNA. ROD 23-MAR-1993 M. MINDEPULS MRNA FOT 19X V(K)MRB11. X63811 S18311 S185174 Immunoglobulin light chain wariable region: monoclonal 19M antibody: VX region.
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Submitted (15-F2B-1995) Jessica H. Roark, Wister Institute,
Spruce St., Philadelphia, PA 19104, USA
Location/Qualifiers
1. 773
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a: 63 c 66 g 76 t
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regions*
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Best Local Similarity 99.3%; Pred. No. 1.38e-109;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps
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223 GGTTCTGGTGTCCCCAAAAGGTTCAGTGCGACTAGGTCTGGTCAGATTATTCTCTCACC 282
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Eukaryotae; m
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Submitted (19-DEC-1991) M. Monestier, Center for Mol. Medicine and Immunology, One Bruce Street, Newark NJ 07103, USA.

(News 1 to 279)
Novick, E., Pasy, T.M., Losman, M.J. and Monestier, M.
Polyreactive 1gM antibodies generated from autoimmune mice and selected for histone-binding activity
1nt. Immunol. 4 (10), 1101-1111 (1992)
See also x63799-019.
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SOUNCE No. Anti-base infochondrial eukaryotes; Netazos; Chordata; Micharyotas; mitochondrial eukaryotes; Netazos; Chordata; Muridae; Eukaryotas; Micharyotas; Micharyotas; Modentia; Sodurognathi, Myomorpha; Muridae; Musicas; Muridae; Muridae; Musicas; Muridae; Muridae; Muridae; Musicas; Muridae; Muridae; Muridae; Muridae; Musicas; Musicas; Muridae; 
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Best Local Similarity 99.3% Pred. No. 1.38e-109;
Matches 150; Conservative ( ) Mismatches 1; Indels 0; Gaps 0;
163 GATTCTGGTGTCCCCAAAAGGTCAGTCGGCTCAGGTCAGATTATTCTCTCACC 222
                                                                                                                                                                                                                                                                                             103 TGGCTTCAGCAGAAACCAAATGAAACTATTAAACGCCTGATCTAGGCGACATCCAGTTTA 152
163 TGGCTTCAGCAGAAACCAAATGAAACTATTAAACGCCTGATCTAGGCAAATCAAGTTA 222
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Nus museulus anti-DNA antibody Ig kappa chain mRNA, V-J region,
Nybridoma 53-46A, partial cds.
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maitted (21-UN-1995) Salah M. Ibrahim, Molecular Biology, Inceton University, Princeton, NJ 05544, USA Location/Qualifiers
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283 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAG 313

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RESULT 11
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bouse mouse.

Mas musculias

Rukaryota, Metasca: Chordata; Verrebrata; Mammalia; Eutheria;

Rodentia; Sciurognathi; Muridae; Murinae; Mu.

Ocomor, Co., Farzell, T.P., Morikava, A. and Stollar, B.D.

Anti-DNA antibodies of normal nice immunized with poly(dC) are
structurally similar to natural autoantibodies

Unpublished
                                                                                                                                                                                              rvovey5 181 bp. mRNA.

Nus musculus dC4 arti-poly(dC) monoclonal antibody kappa light chain variable region, (IgK) mRNA, partial cds.

AF045495
92906073
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	source
Medicine, 136 Harrison Avenue, Boston, MA 02111, USA	FEATURES
Submitted (02-FEB-1998) Biochemistry, Tufts University School of	JOURNAL
Direct Submission	BITTE
O'Connor, K.C., Farrell, T.P., Norikava, A. and Stollar, B.D.	AUTHORS
2 (bases 1 to 381)	REFERENCE
Unpublished	JOURNAL
structurally similar to natural autoantibodies	
Anti-DNA antibodies of normal mice immunized with poly(dC) are	TITLE
O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D.	AUTHORS
1 (bases 1 to 381)	REFERENCE
modernian, orangement, merande, merande, mes.	

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/genewigk
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chain
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CDS gen

BASE COUNT J\_segment V\_region sig\_peptide /gene="IgK"
61. .345
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346. .>381
/gene="IgK"
93 a 90 c

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223 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAG 253

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89 g 109 t

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Overy Match 27.6; Score 170: DB 29; Length 381; Best Local Scillarity 93; Fred No. 138-109; Indels 0; Gaps Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps

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Page 37

US-08-836-455-1.rge

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Page 38
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REYWORDS C-region; V-region; immunoglobulin light chain; immunoglobulin kappa.

SOURCE Kunuse 4 week old spleen B cell hybridoma, cDMA to mRNA, clone 52-14.2

ORGANISH week old spleen B cell hybridoma, cDMA to mRNA, clone by musculus bloodomaid subaryotes; Metazod, Chordata; werebatte but bereia; Rodentia, Sciurognathi, Myomorpha, Muridae; werebatte to 10 millione; Nus Buridae; huridae; huridae; Nus Hurid
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KEYNORDS house mouse.
SOURCE Nouse muselius
ORGANISM Hus museulius
Enkaryotas: mitochondrial eukaryotes: Metasoa; Chordata;
Vertebrata: Eutheria; Rodentia; Solurognathi; Muridae; Murinae;
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223 GGTTCTGGTGTCCCCANANGGTENAGTGGATANGGTCTGGTCAGATTNTTCTCTAACC 282
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SKIRANAN, K.R., Jou, M.-T. and Marion, T.N., CDR3 structures and specificity for DNA among autoimmune antibodies to DNA 1 immunol. (1997) In press

2 (bases 1 to 328)

Direct Submission

15 Direct Submission

16 Marion, 7.N. (18-PAR-1996) Tony N. Marion, Dept. of Microbiology/immunology, University of Tennessee, 858 Madison Ave., Memphis, 738 8183; DOS (1907) Marion, Dept. of Memphis, 738 8183; DOS (1907) Marion, Dept. of Memphis, 738 8183; DOS (1907) Marion, Dept. of Memphis, 738 818; DOS (1907) Marion, Dept. of Memphis, 
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             Location/Qualifiers
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/PCOUCCE-'AMBURGOS|DEULIN ABPRA-CHAIN VN-1"
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/TERNALALION-'ESPESIGASIGENTSLICEASODIGNSLAHIQOEDGTINALIY
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283.331

BASE COUNT 81 genes*1gA*
ORIGIN Chromosome 6. 79 c

Query Match
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SOURCE DOUGH musculus immunoglobulin light chain; immunoglobul more mouse.

ORGANISM Ms musculus mitochondrial eukaryotes; Metasoa: Ch. Eukaryotes: mitochondrial eukaryotes; Metasoa: Ch. Eukaryotes: mitochondrial eukaryotes: Metasoa: Ch. Eukaryotes: mitochondrial eukaryotes: Metasoa: Ch. Mitochondrial eukaryotes: Mitochondrial eukaryotes: Metasoa: Ch. Mitochondrial eukaryotes: Mitochond
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Best Local Samilarity 99, Be, Pred. No. 2, SSer 87;
Matches 161; Conservative 0, Mismatches 2; Indels 0; Gaps 0;
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Best Local Similarity 97.2%;
Matches 138; Conservative
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                                                                  MUSEX BD BRUA RD 07-JAN-1997 Mus Phus-culus (cell line C3H/P2-15) chromosome 6 anti-DNA antibody 149ht chefs; chain mRNA.
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Specific for influence virus A/PR/8/34 hemagglutinin.
Location/Qualifiers
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Catom.A.J., Stark,S.E., Kavaler,J., Staudt,L.M., Schwartz,D. and Gerhard, M.
house mouse.
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/dev_stage="4 week old"
/tissue_type="splenic hybrydoma"
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Mus musculus Bukaryotae, micochondrial eukaryotes, Hetazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Huridae;

Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Murinae; Mus. 1 (Dases 1 to 305) Hesthoff,C.M., Wylie,D.E., Kathol,S., Whittier,A., McHugh,J. and Shultz,L.D.

Viable motheaten anti-DNA antibody

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311 TAGCCTATTACTGTCTACAATAGCTAGTGTCCGTACACGTCGAGĞĞĞĞACCAAGC 370
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Rusaryota: Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

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1 (Chases 1 to 381)

Chases 1 to 38
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Mon Apr 19 13:23:48 1999
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AUTHORS
JOURNAL
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ORGANISM
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LOCUS
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COMMENT
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Best Local Similarity 99.2%; Pred. No. 7. 80e-84;
Matches 128; Conservative 0; Mismatches 1; Indels 0; Gaps
                                                                                                                                                                                                                                                   sig_peptide
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| 148 GGTA 151
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||||||||
283 ATCAGCAGC 291
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223 GGTTCTGGTGTCCCCAAAAGGTTCAGTCAGTCAGTCTGGGTCAGATTATTCTCTCACC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 TCCTTATCTCCCTCTCGGAGAAGAGTGAGTGACTTCATGTGTGGGGGAAGTGAGGACATT 147
88 TCCTTATCTGCCTCTCTGGGAAAAGAGTGAGTCTCATTGTGGGGAAGTTAGGACATT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
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Nue musculia (strain BALB/c, sub_species domesticus) cDNA to mRNA.

Mus musculia (strain BALB/c, sub_species domesticus) cDNA to mRNA.

BUARTYOTEE: pitchonds:-1 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WISIOKONK 456 bp mRNA ROD 26-MAR-1994 NOLES IS TEATRANGED ARPPA-Chain mRNA, clone AN12K.
M19914 070352
C-region; immunoglobulin light chain; immunoglobulin-banna.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (Chaese 1 to 306)
Westhoff,C.M. Wylie,D.E., Rathol,S., Whittier,A., McHugh,J.
Binltz,L.D.
Direct Submission
Submitted (06-FEB-1997) Biological Sciences, University of
Nebrasks, 335 Kanter Hall, Lincoln, NE 65588-0118, USA
Location/Qualifiers
1. 306
1. 306
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2 (base 1 to 455)

2 (base 1 to 455)

3 (base) 1.7 Rule, G. 9. Whittaker, M. M. and McConnell, H. M. Sequence of 12 monoclonal anti-dinitrophenyl spin-label anti-bodies for Nam studies

Proc. Natl. Acad. Sci. U.S.A. 85, 3661-3665 (1989)

8073/466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry and computer-readable sequence [2] kindly submitted by e, 20-JUL-1988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yotae; mitochondrial eukaryotes; Metazoa; Chordata;
brata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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sed gene.
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/strain="viable motheaten"
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/sub_species="domesticus"
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/prduct="anti-DNA antibody light chain variable region"
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/prduct="spn:q305113"
/ranalation="GPSSLASICERVSLICENSQDIGSSLNHLQQEPOGIRALIY
ATSSLDSGVPRRPSGSRSGSDYSLTISSPESEDFVDYYCLQYASSPWTFGGGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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Mon Apr 19 13:23:48 1999
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BASE COUNT ORIGIN

mat\_peptide

Cuery March 20.9%; Score 91; DB 29; Length 456; Best Local Similarity 100.0%; Pred No. 9.75e-76; Indels 0; Gaps Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps

ACCESSON USS617V
REPMONS 988617V
REPMONS NOME mones
ORGANISH Mus muser.
Enteryotae; mi
Vertebrate: E

mitochondrial eukaryotes: Metazoa; Chordata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

Hurine: Mus.

CE Insekins. M. Weigert, M. Basu.C., Erikson, J. and Radic, M.E.

E. Licht, tohis on the part of specificity in anti-DNA antibodies

M. J. Immunol. (1995) In press

M. J. Immunol. (1995) In press

M. Z. (hase 1 to 593)

DES Insekins, S. M., Meigert, M., Basu.C., Erikson, J. and Radic, M.E.

E. Direct Suminasion

B. Direct Suminasion

B. Sumnitted (32)-UN-1995) Saleh M. Ibrahim, Molecular Biology,

M.L. Sumnitted (32)-UN-1995) Saleh M. Ibrahim, Molecular Biology,

M.D. Sumnitted (32)-UN-1995, Male Muserial Molecular Biology,

E. S. Location/Qualifiers

Location/Qualifiers

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CDS

Action in the water for the form of the fo

RESULT 21 LOCUS DEFINITION

hogi3018 293 bp meBah Mus musculus anti-DNg antibody Ig kappa hybridoma 84.32, partial cds. U30236 g895.70

ROD 18-OCT-1995 chain mRNA, V-J region

223 A 223

le 91..>456 /product="immunoglobulin kappa-chain" 118 a 114 c 108 g 116 t -----

US-08-836-455-1.zge

Page 45

Mon Apr 19 13:23:48 1999

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/translation="XYLMTOYPSSIGASIGERVSLTCRASGDIGSSLWMLQQEPDGTI
KKLITATSSLDGOPKRFSGSRSGSDYSLTSSSLUSEDFTDYSCLQTASSFWNV"
72 a 71 c 66 g 82 t 2 others
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Page 46

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Query Match 20.7s, Score 99; DB 39; Length 293; Best Local Similarity 99.2s; Pred No. 138e-74; Best Local Similarity 99.2s; Pred No. 138e-74; Indels 0;
                                                               103 TOGETTCACCAGANCCACTGATCANCTANCCCCGATCTANCGCCACTCACTTTA 162
Gaps
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NETWOODS STATEMENT OF THE PROPERTY OF THE PROP
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DEFINITION Sequence
ACCESSION 132991
NID 91823782
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Lence 45 from patent US 5589573.
Score 90; DB 22;
Pred. No. 1.38e-74
0; Mismatches
0; Indels 0;
                                                                                                                     Length 438
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base sequences
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334 PROCOTTOGRAGGGGARCAMGTGGAMATAMANGGGCTGATGCTGCACCAACTGTA 393
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Apr 19 13:23:48 1999
US-08-836-455-1.rge
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Page 47

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8888888888888888888888888
/organism="Mus musculus" | O other: Sequence 438 BP; 104 A; 120 C; 112 G; 102 T; 0 other:
                        Bource
                                                                                                                                                                    misc_feature
                                                                         misc_feature
                                                                                                      misc_feature
                                                                                                                                     misc_feature
                                                                                                                                                                                                   misc_feature
                                          /note**Fragment 4 of light chain variable region of idio17*
Location/Qualifiers
                                                                                                        region
                                                                                                                                                                      /154...198
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199...219
                                                                                                                                                                                                   /note="CDR1 of light chain wariable region Idiol?"
154. .198
                                                                                         220. 135
Protes Fragment 3 of light chain variable
region of Idiol?
15. 139
16. 139
17. 139 of light chain variable region
                                                                                                                                               Idio17
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[dio17"
340. .369
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Query Match
Best Local S
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20.7%; Score 90; DB 10; Length 438; Similarity 100.0%; Pred. No. 1.38e-74; Score 90; Conservative 0; Mismatches 0; Indels 0;
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334 TRANCOTTICGAGGGGGACCIAGCTGAMATAMACGGCCTATGCTTGCACCAACTCTA 393
346 TRANCOTTICGAGGGGGGACCIAGCTGGAMATAMACGGCCTATGCTGCACCACTCTA 405
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REPORDS

ACTIVITIES

ORGANISM Manusculus

ORGANISM Enterpotes: Metazoa: Chordata; Vertebrata; Manusalia; Entheria;

REPERENCE 1 (bases 1 to 570)

AUTHORS Ultich, H. D., Moore, P. L. and Schultz, P.G.

TITLE Germline diversity within the mouse Igk-V9 gene family

TOURNAL Immunogenetics 47 (1), 91-55 (1998)
                                                                                                                                                                            ACCESSION
NID
                                                                                                                                                                                                                  RESULT 24
LOCUS
DEFINITION
                                                                                                                                                                        AF003293
Mus musculus
cds.
AF003293
92306844
                                                                                                                                                                                                                  570 bp DNA
Ig kappa light
                                                                                                                                                                                                                  ROD
chain variable region
                                                                                                                                                                                                                24-JAN-1998
gene, partial
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394 TCCATCTTCCCACCATCCAGTAAGCTTGGG standard; RNA; ROD; 438 BP. 435

423

GioCri-1997 (Rel. 52, Created)
08-OCR-1997 (Rel. 52, Late updated, Version 1)
08-OCR encoding light chain variable region of muse antiidiotype
antibody named 1ddo17 espainst CHF-196 idiotype.
197 1995101999-A/7.
Nus musculus (Douze mouse) . Vertebrata; Mammalis; Eutheria; Rodentia;
printroynethi; Muridae; Muridae; Muridae; Mus.

DESIGNATE H., ADRING Y.;

MAINO ACID SEQUENCE OF ANTI-IDIOTYPE ANTIBODY TO ANTI-CANCER HUMAN MAINO ACID SEQUENCE CODING FOR THE SAME';

RECHI (number UP 195101399-A/7), 18-APR-1995.

MAINO ANTIBIDE.

MAINO MAINO MAIND MAINO MAIN

strandedness: Double: topology: Linear: hypothetical: No: anti-sense: No: Key source 1. 438
/organism\*Mus musculus\*
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/clone="17KB1"
1. 39
40. 438 Location/Qualifiers

sig\_peptide mat\_peptide

misc\_feature

misc\_feature

Query Match 20.7%; Best Local Similarity 100.0%; Matches 90; Conservative

394 TCATCTTCCCACCATCCAGTAAGCTTGGG 423

MEDLINE REFERENCE AUTHORS TITLE JOURNAL

98044209

ORGANISM

Mus musculus Eukaryotae; p

mitochondrial eukaryotes; Metazoa; Chordata; Butheria; Rodentia; Sciurognathi; Myomorpha; Muridae;

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LOCUS
DEFINITION
ACCESSION
NID
KEYWORDS
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NID
KEYWORDS
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// gene=1gk*
601. 628

// gene=1gk*
602. 628

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Best Local Similarity 98; Pred. No. 1.95e-73;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Best Local Similarity 90.7%, Pred No. 1.95e-73; Indels 0; Gaps
Matches 149; Conservative 0; Mimmatches 2; Indels 0; Gaps
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                                                                                            sig_peptide
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223 GGTTCTGGTGTCCCAAAAGGTTCAGTGCAGTAGAGTCTGGGTCAGATTATTCTCTCACC 282
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163 TGCCTTCHCCAGANCCACATCGANCTATTALACCCCTCATCTACCCACACACCAGTTA 222
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germ line; Ig kappa light chain; immunoglobulin; signal peptide.
house mouse.
Mus musculus
Eukarpotas; mitochoidrial eukaryotes; Metaróa; Chordata; !
Verteara, Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUSICKVE 664 bp DNA 25-APR-1996
MOUSE IS Mappa germline V gene: VK41. ROD
100566
g197441
C region; V-region; complementarity determining region; framework
region; germline; hypervariable region; immunoglobulin light chain;
immunoglobulin kappa; immunoglobulin kappa subgroup vk-9.
kus museculius emboryo DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (base 1 to 570)
Ulrich H.D. and Schults,P.G.
Direct Submission
Submitted (09-MY-1997) 2x8H, Universitant Heidelberg, Im
Neuenheiner Feld 282, Heidelberg D-69120, Germany
Location/Qualifiers
1. 570
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1 (base 1 to 664)

2 (base 1 to 664)

3 (sidman,7:6., Max.E. and Leder,P.

3 (sidman,7:6., Max.E. and Leder,P.

3 (sidman,7:6.)

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/gemline
/
                                                                                                                                                                                                                                                                                             the the earlier entry <MMIG20>
                       /organism="Mus musculus"
/db_xref="taxon:10090"
120. 173 |
/note="first exon (leader)"
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/*strain**BALBAC; A.V.; Sviss Webster*
/*tissuc_type="liver"
/*cil_line**MOPC41*
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BASE COUNT
ORIGIN
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MUSICIAPA 618 bp mRNA. ROD 09-JUL-1996
DEFINITION Hopes aRNA for immunoglobulin light chain, partial sequence.
ACCESSION 947956
EXPRORES 1947956
SOURCE MALE MANUAGE 1945 Chain
ORGANISH Has musculus (sub_species:domesticus, strain:BALB/c) CDNA to mRNA.
DRAMPORES Has musculus (sub_species:domesticus, strain:BALB/c) CDNA to mRNA.
EXPRORES Has musculus (sub_species:domesticus, strain:BALB/c) CDNA to mRNA.
Verrebreaks Mammalis: Eutheria: Rodentia: Sciurognathi: Muridae;
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Best Local Similarity 98.7%;
Matches 149; Conservative
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163 TCCCTTCACCACCAACCAATCGATCTATTAAACCCCTGATCTACCCCACATCCACTTTA 222
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RS Setdamin, J.G., Max, E. and Leder, P.

A kappa Laminopibblin gene is formed by site-specific remains and included in the common set of the common set
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/codon_start=1
/product=tapp.immnoglogulin*
/product=tapp.immnoglogulin*
/db_start=1
/timal_station=*Nutwaba01FGFLLLEFOGTRCDIONTGSPSSLANSIGERVSLT
CRASQDIGGSLMFLQGEPOGTIKRLITATSSLDSGVPKNFFGGSRSGSDYSLTISSLES
EDWTYTCLGTASSP
100. 139 g 2n. -
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join(120...174,303...313)
/gene*igx
/note**VX1*
join(120...174,303...598)
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'db_xref="taxon:10090"

'dev_stage="embryo"
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Pred. No. 1.95e-73;
0; Mismatches 2; Indels 0; Gaps
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Page 54

Gaps

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RESULT 30
LOCUS MANU24115 471 bp mRNA
DEFINITION Mus musculus immunoglobulin MCCESSION U24115
NID 9777412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 CTOCGTACHOCTTOGRAGGGGGACCARCCTGGAAATAAAACGGGCTGATGCTGCACCAA 314
house mouse.
Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metasoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
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2 (bases 1 to 438)
Schoppel, K.
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Sindhitted (92-MOV-1995) Michael Mach, Institute of Virology,
Submitted (92-MOV-1995) Michael Mach, Institute of Virology,
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Nus musculus
Eukaryotae; micochondrial eukaryotes; Netazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Schoppel, K., Hassfurther, E., Britt, W., Ohlin, M., Borrebacck, C.A.
and Mach, M. Hassfurther the antigenic domain 1 of glycoprotein B
Antibodies apecific for the antigenic domain 1 of glycoprotein B
(gpUISS) of human cytomegalovitus bind to different substructures
virology 216 (1), 133-145 (1896)
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/Product*=ait.iglycoprotein-B of human Cytomegalovirus
immunoglobulin VI chain*
/db_xref.**PID:g1680675*
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/strain="BALD/c"
/sub_species="domesticus"
/db_xref="taxon:10090"
<1. .>618
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/strain="Salb/C"
/note="monoclonal antibody 27-287*
/db_xref="taxon:10090"
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//db_xred="PID:q473961"
//db_xred="PID:q
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F9.13.7 light chain mRNA, partial cds
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SOURCE
House mouse.

ORGANISH Mas muscults

Enkaryotes, micochondrial eukaryotes; Metasoa; Chordata;
Enkaryotes, Micochondrial eukaryotes; Metasoa; Chordata;
Periebrata; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Best Local Similarity 100.0% Pred No. 7.57e-69; Length 471;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps
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Leacar J. Pollogini M., Souchon H., Tello,D., Poljak,R.J.,
Peterson N.C., Greene M. T. and Altari P. Milo,D., Poljak,R.J.,
Crystal structure of a cross-reaction complex between Pab F9.13.7
and Gainaa-fowl lyackyme coss-reaction complex between Pab F9.13.7
J. Biol. Chem. (1995) In press
2 (bases 1 to 471)
Person. N. T.
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Schoppel,K.
Direct Submission
Submitted (07-WOV-1995) Michael Mach, Institute of Virology,
Submitted (07-WOV-1995) Michael Mach, Institute of Virology,
Onlyezaty Criangen-Nurmberg, Schlossgarten 4., 91054 Erlangen,
Germany
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Schoppel, K., Hassfurther, E., Britt, W., Ohlin, M., Borrebaeck, C.A.
and Mach, M.
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Dmitted (01-MPR-1995) Norman C. Peterson, Pathology and
Dboratory Medicine, University of Pennsylvania School of Medicine,
31 John Morgan Bidg., 38th St. and Hamilton Walk, Philadelphia, PA
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/Produce*_mit_glycoprotein-B of human Cytomegalovirus
/Produce*_mit_glycoprotein-B of human Cytomegalovirus
/Produce*_mit_glycoprotein-B of human Cytomegalovirus
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/codon_gtart=1
/product='immunoglobulin F9.13.7 light chain'
/db_uret='PID:g77413'
/db_ure
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/strain="BALB/c"
/db_xref="taxon:10090"
/cell_type="lymphocyte/hybridoma"
<l...>471
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/db_xref="taxon:10090"
1. .>423
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strain="Balb/C"
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Pred. No. 7.57e-69;
0; Mismatches 0; Indels 0;
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RESULT 28
LOCUS
DEFINITION

REFERENCE AUTHORS

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KEYWORDS SOURCE ORGANISM ACCESSION NID

RESULT

31

KEYWORDS SOURCE ORGANISM

BASE COUNT ORIGIN

SG

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Apr 19 13:23:48 1999

Matches

85; Conservative

0; Mismatches 0; Indels 0; Gaps

RESULT 32
LOCUS
DEFINITION

MCM73895 642 bp mRNA ROD 08-0CT-1996 Nus musculus MabB9 anti-spolipoprotein B-100 Ig kappa light chain mRNA, partial cds. U29869 91633778

oclonal antibody; cDNA; apolipoprotein B-100: low-density

403 TGTATCCATCTTCCCACCATCCAGT 427

ACCESSION NID REYWORDS

SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae:

REFERENCE AUTHORS

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LOCUS
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Best Local Similarity 100.0%;
Matches 85; Conservative
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                             NISM Notes Bouse.

NISM Nue manchine

Pikaryotes introhondrial enkaryotes Metasca: Chordata:

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house mouse.
Mus musculus
Sukaryotas; mitochondrial eukaryotas; Netazoa; Chordata;
Dukaryotas; mitochondrial eukaryotas; Netazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Schurognathi; Nyomorpha; Muridas;
Vertebrata; una
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M.musculus WM65 kappa immunoglobulin mRNA.
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265. _291
/note="encodes CDR3"
322. _>642
188 a 152 c 152 g
rect Submission
bmitted (22-MAR-1995) Andreas G Plueckthun, Biochemisches
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nitted (08-FEB-1991) R. Seymour, Haematology Dept, St Vincents
pital, Victoria St, Sydney NSW 2010, Australia
Diages 1 to 593)
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/strain="BALS/c"
/db_xref="Exxon:10000"
/tissue_type="haemapoietic"
/cell_type="bloid/hybridoma"
/clone="FUC18"
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/note="
347. .3
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/note="J region"
383. .593
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148 .. 168
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VILTPYLIPGGEPOLLI INAANAN TYSI EPPSSEQLISGIAS VUGELARIY
KILDSERONGVILAN TANDAN TYSI EPPSSEQLISGGAS VUGELARIY
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378 TGTATCCATCTTCCCACCATCCAGT 402

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Submitted (12-UN-1995) Ju-Won Kvak, Korea Research Institute of Bloselence & Elotochology, Protein Engineering Group, Yuseong, Taejon, 195-500, Korea Buharyotas: mitochondrial eukaryotes: Hetaros: Chordata: vertebrata: Eukheria; Rodentia; Sciurognathi; Hyomorpha; Huridae; Murinae; Mus. 100 642)

Norda, 100 642

Norda, stitut, Universitate Euerich, Winterthurerstr. 190, Zuerich, 18057, Switzerland
(base 1 to 681)
L., Lupes A., Persidi-Boux S., Spads, S. and Pluckthun, A.
L., Lupes A., Persidi-Boux, S., Spads, S. and Pluckthun, A.
Deciding the propertied of very unusual framework structure loses mortion when converted to the consensus.

Bioli Chem. 270 (21), 12446-12451 (1995) /notem=3 bases missing compared to kappa consensus sequence:
214. 246 /poduce-timminoglobulin light chain (Y-J and kappa
content chilin
content chilin /organism="Mus musculus" /strain="BALB/C" /db\_wref="taxon:10090" ...25 Cocation/Qualifiers Organiam "Mis musculus"

Abbare' Taxon: 1000'

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Albare Type' Typhony te-Sp2/O myeloma' evidence-experimental untion-Fpb fragment of the antibody 91-6, which binds otherible coli tryprophen synthese vibt DD = 6, or at the "The heavy chain of this antibody is a normal member the murine Vs a subgroup. This kapp 14pht phath has an Extince vs. 8 antibody is and a deletion framework-2 which converted to the consensus, it loses tigen binding function\* oots"encoded by the PCR primer. The true sequence may us be somewhat different in this region" 6. .681 on/Qualifiers US-08-836-455-1.rge

MEDLINE REFERENCE AUTHORS TITLE

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PEATURES source mRNA CDS intlisequences from myelomas mopelis, hpc76, and mepc603 are intlisequences from myelomas mopelis, hpc76, and mepc603 are main declevith this locus event loough they are different from the main declevith by a control of their main declevith of their main declevith of their main is unusual in that a productive rearrangement of myeloma mappel. The Y untranslated region (Y ut) of the mappel main is unusual in that it probably consists of only the mappel main is unusual in that it is probably consists of only the mappel myeloma mappel. The Y untranslated region (Y ut) of the mappel myeloma mappel, the same late y that has a lap of the mappel myeloma mappel, that is further supported by the discovery of another kappa y gene which has a lap y ut a correct. This is further supported by the discovery of another kappa y gene which has a lap y ut a correct myeloma mappell has not been sequenced. The general myelomatic region of mappell has not been sequenced its joining causalyers for germline kappa wariable regions; see loci beginning causalyers for germline kappa wariable regions; see loci beginning causalyers for germline kappa wariable regions and see loci beginning causalyers for germline pape wariable regions; see loci beginning causalyers for germline pape wariable regions for the kappa genes, and see loci beginning causalyers for germline policing and constant the first scale correct page was a second to general type genes and see loci beginning causalyers for germline policing and constant type for the kappa genes and see loci beginning causalyers for germline policing and constant type genes and the completion of the second page genes and see loci beginning causalyers for germline general page genes and see loci beginning causalyers for germline may be under the general part of the second page genes and see loci beginning causalyers for general genes and see loci beginning causalyers for general gener 6 (Date 1 to 943) 8mm/yn.P.H., Gait.M.J. and Milstein,C. Complete sequence of an immunoplobulin mRNA using specific prining and the disexpruciecise method of RNA sequencing MICHAEL ACIDS RES. 9, 4485-4494 (1981) 80059479 nouse cdna to myeloma mopcil mrna [1], [3]; cdna to myeloma p3 (detrived from mopcil) mrna [2], [5], [6]; cdna to myeloma mopcil) mrna; cdna to myelomas mopcila, mcpc603, s107 & hpc76 mrna [5]. Location/Qualifiers /organism="Mus musculus" /db\_xref="taxon:10090" |. .943 'note='kappa mopc21 mRNA'
1. /35
'note='kappa mopc21 coding sequence'
'codon\_start=1
'db\_xref='PID:9309359'

Mon Apr 19 13:23:48 1999 V\_region CDS 'organism="Mus musculus"
'db\_xref="taxon:10090" US-08-836-455-1.rge

Page 63

luct="variable region of Ig kappa light chain" '35

/product\*\*constant region of 1g kappa light chain\*

BASE COURT 255 a 255 c 206 g 227 .

ORIGIN /codon\_start=1
/product="munoglobulin kappa light chain"
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Oury Match 19.5%; Score 85; DB 29; Length 943; Best Local Stallarity 100%; Pred No. 7.57s-69; Length 943; Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 372 TOGTHANGSTROAGGGGGGGGGCANGTRGANATHANGGGGCTGATGGTGGACGAG 431
342 TOGTHANGSTTCGAGGGGGACCHACTGGANTHANGGGGCTGATGGTGGACGAG 401

AID
KETWORDS

house mouse.

ORANISH Kus musculus

Dikaryotes; mitochondrial eukaryotes; Hetazoa; Chordata;
Eukaryotes; Eukaryotes; Murinae;

Verrebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; RESULT 36

LOCUS MUD68543 1101 bp mRNA ROD 16-SEP-1996

DEFINITION M4s machine Ig single-chain antibody mRNA, complete cds.

ACCESSION 06843

ACCESSION 06843

ACCESSION 071547272 1 (Lease 1 to 1101) Manon, P.W. Berinstein, A., Baxt, B., Parsells, R., Kang, A. and Rieder, E. Cloning and expression of a single-chain antibody fragment specific for foot-and-mouth disease virus

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09 342 TCCTRANGTTCGAGGGGGACHAGTGGAAATAHAACGGCTGATGCTGCACHAG 401
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LOCUS 107388 639 bp
DEFINITION Sequence 3 from Patent EP 0338767.
ACCESSION 107388
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Best Local Similarity 100%; Pred No. 7.57e-69;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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2 (bases 1 to 1001)

Resent Submitted (10-AUG-1996) Peter W. Mason, Foot-and-Mouth Disease
Submitted (10-AUG-1996) Peter W. Mason, Foot-and-Mouth Disease
Research Unit. USBA/ARS/WAA/PIADC, Greenport; WY 11944, USA
Location/Gualifiers

ee
Nus musculus
Mus musculus
Bukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Schurognath; Muridae; Murinae; Mus.
1 (bases 1 to 321)
Ulrich, H. D. and Schultz, P.G.
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1 (bass 1 to 539)

Reavers_L.S., Bumol.T.P., Gadaki,R.A. and Weigel,B.J. hovel recombinant and chimeric antibodies directed against a human adenocarcinoma antigen
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RESULT 40 LOCUS DEFINITION ACCESSION NID	рь 230 g Qy 290 g	рь 170 с Qy 230 с		BASE COUNT ORIGIN	CDS	Bon	REFERENCE AUTHORS TITLE JOURNAL FEATURES	REPERENCE AUTHORS TITLE JOURNAL MEDLINE	JOURNAL	Apr 19		<b>498</b>	AUTHORS	REPERENCE	ACCESSION NID KEYWORDS SOURCE	RESULT 38 LOCUS DEFINITION	рь 340 с Оу 403 с	рь 280 с Qy 343 с	Query Match Best Local Matches		JOURNAL FEATURES
40 MRG5052 379 bp mRNA, ROD 19-FEB-1997 NN Mus musculus polyreactive autoantibody, immunoglobulin light chain kappa mRNA, partial cds. 7 052052 91438594	GCCTTGAGTCTGAAGATTTTG 310	OTOTOCCCMANAGOTTCAGTGGGGTGAGATTATTCTCTCACACATCAGCA 239	18.6%; Score 81; DB 29; Length 321; similarity 100.0%; Pred. No. 2.79e-64; Onservative 0; Mismatches 0; Indels 0;	89	/call_type="hybridona" /folia_type="hybridona" /folia_		B (Dases 1 to 321) 5 Ulrich; H.D. and Schulter, P.G. Direct Submission L Submitted (09-MAY-1997) ZMSH, Universitaet Heidelberg, Im Reuenheimer Feld 282, Heidelberg D-69120, Germany Reuenheimer Feld 282, Heidelberg D-69120, Germany	2 (bases 1 to 321) Ulrich, H.D., Moore, F.L. and Schultz, P.G. Germline diversity within the mouse 19k-v9 gene family Immunogenetics 47 (1), 91-95 (1998) 9804209	Structure-function relationships in a family of catalytic antibodies	3:23:48 1999 US-D8-836-455-1.rge		complexes Upublished Upublished 2 (bases 1 to 436) Dailtis B		x Mus musculus Rukaryota; Metaroa; Chordata; Vertebrata; Mammalia; Eutheria; Rodenia; Sciurognathi; Muridae; Murinae; Mus.	A NO1256 g1860516 immunoglobulin superfamily; kappa chain; variable region. house mouse.	38 MMO012555 436 bp mRNA procific immunoglobulin, kappa chain, variable region, partial.	GRATICANOPTICOACCANICANO 363 [	CCCTACACCTTCCACCCCACCCACCCACCTGAAATAAAACCCCCCTACTCCTCCACCAACT 339	atch 19.18; Score 84; DB 22; Length 639; call of the constrainty 100.08; Pred. No. 1.05=-67; Indels 0: Gaps 0; 84; Conservative 0; Misaktives 0; Indels 0: Gaps 0;	174	

OURCE house mouse.	Apr 19 13:23:48 1999
	#7.4 25.4

US-08-836-455-1.rge

Mon Apr 19 13:23:48 1999

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Page 70

en.M.I., Saviranta,P. and Karp,M. Ammunoglobulin aberrantly rearranged kappa-chain-mRNA

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Best Local Similarity 100.0%;
Matches 81; Conservative
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319 TACACCTTOGRAGOGGGACCAMGCTGGAMATAMACGGGCTGATGCTGCACCAMCTGTA 378
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Rus muculus
Eukaryotae: mitochondrial eukaryotes: Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae: Mus. 4821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAIGLEAM 882 bp RNA ROD 30-SEP-1993 M. HUMBOULE BRNA for monoclonal antibody light chain kappa. 370424 9406554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryotes: Metazoa; Chordata; vertebotata; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (Dases 1 to 379)
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Submitted (15-70W-1996) Laboratoire d'Immunohematologie et
d'Immunopathologie, Datieut Pasteur, 28, rue du Dr. Roux,
75724 Paris Cedex 15, France
Location/Vualifiers
1. 7379/Qualifiers
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Dlav L., Magnac,C., Pritsch,O., Buckle,M., Alzari,P.M. and
Dighiero,G.
Structural and affinity studies of IgN polyreactive natural
autoantbodtes
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/TERBALATON**NILTOPASSLAVSLGORATISTRASKSVSTSGYSTKHWNQRP
GOPPRILTIUNSWIESGVPRRESGGGGTDFTLMIHPVEEDNATTYCGHIRBATTYG
GGTLEHIRADAJPVSIPPSSE;
96 a 104 c 92 g 87 t
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itero,G.
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355. 675
/note="CL domain"
a 241 c 194 g
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                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/product='immunoglobulin light chain kappa*
/b_xred='pig-166255*
/tanslation='VFLLCYSGAHGSIVENGTERFILEADDRYITEKASGSVEND
VARTOGNEGGFREITYNSSRYTGVFDREFTGSSTETTFFTSTTYQLEULAVENGU
VARTOGNEGGFREITYNSSRYTGVFDREFTGSSTETTFFTSTTYQLEULAVENGU
DESETTFGGGTTLEIKADAA,PTVS:FPPSSEQLISGGASVYGFLNETYEDINVIN
IDGERONVIJNSFTDQDSKDSTYSMSGTLTLTKDEFERHNSTTCEATHKTSTSPIVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organisme"Mus musculus"
straine "balb/c"
db_xref="taxon:1000"
cell_type="hybridoma cells"
cell_tine="N alpha 2-3"
tlong="No. 26"
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/product="polyreactive autoantibody, immunoglobulin light
chain"
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/Attain (CDA/NRSALM/C)Fl:
/Actain (CDA/NRSALM/C)
                                                                                      Score 81; DB 29; Length 882;
Pred. No. 2.79e-64;
0; Mismatches 0; Indels 0; Gaps 0;
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                                                                                                                                                              BASE COUNT
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KEWNORDS
SHORE MOUSE.
ORGANISH Mus musculus

Eukaryotas: misochondrial eukaryotas; Metazoa; Chordata;
Vertebrata; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae;

Vertebrata; Mus.
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US6414 97072142
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396 TOCATOTROCOACCARCCAGT 416 316 TACACCTTCGAGGGGGACCAACCTGAAATAAAACGGGCTGATGCTGCACCAACTGTA 385 Similarity 100.0%; Psecd: 81; DB 29; Length 729; Similarity 100.0%; Psecd: No 2.79e-64; DB 29; Conservative 0; Mismatches 0; Indels 0; Gaps /product="Vk segment" 197 a 197 c 178 g /organism="Mus musculus"
/db\_wref="taxon:10090"
/cell\_line="Rybridoma cell line WIS 1186"
11. 369 (22-APR-1996) M.I. Pajunen, Turku Centre for 597. P.O.Box 123, Turku FIN-20521, Finland L. Kol. Immunol. 35, 991-995, 1988 Gene 123, 321-328, 1992. vokion/Qualifiers don\_start=1
reption="No explanation supplied"
redo Saviranta,P., Jauria,P., Karp,M., Pettersson,K., d\_Lovgren,T. 157 t

Mon Apr 19 13:23:48 1999 US-08-836-455-1.rge

REYMONDS 1901; kappa chain; light chain; variable region. SOURCE house mouse. ORGANISH Mus musculus MMIGGIVI 330 bp DNA ROD M.musculus IgG1, light chain variable region. X82890 karyotae; mitochondrial eukaryotes; Metazoa; Chordata; rtebrata; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; 02-SEP-1996

1 (bases 1 to 330)
Revario-Teulon, T., Peraldi-Boux, S., Bernardi, T., Marin, M.,
Plechneryk, M., Shire, D., Pau, B. and Blard-Piechneryk, M.
Supression in Eacherichia coli of soluble and M13 phage-displayed
forms of a single-robhin antibody fragment specific for dispariaimmunotechnology 1 (1), 43-52 (1993)
18040653 rractum: (Published erratum appears in Immunotechnology 1995 ec; (2-4): 243-4]
(Pases 1 to 310)
avarro-Teulon, 1.
trect Submission
ubmitted (33-W07-1994) I. Navarro-Teulon, CNRS UMR 9921 Faculte
harmacie, 25 Avenue Charles Flahault, P-34060 Hontpellier Cedex
1. PRANCE

ocation/Qualifiers

/organism="Mus musculus"
/organism="Mus musculus"
/otasue\_type="hybridoms"
/olones\_TCD hybridoms"
/olones\_TCD hybridoms

174 CCCCMANGGTTCAGTGGGGCAGAGTTATTATTCTCTCACCATCAGCAGCT 233 h 18.4%; Similarity 100.0%; 80; Conservative Score 80; DB 29; Length 330; Pred. No. 3.83e-63; 0; Mismatches 0; Indels 0; Caps

Ş	B	Apr
294 TGAGTCTGAAGATTTTGTAG 313	234 TGAGTCTGAAGATTTTGTAG	n Apr 19 13:23:48 1999
313	253	g <del>e</del> n
	-	US-08-836-455-1.zge

Mon Apr 19 13:23:48 1999

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Best Local Similarity 100.0%; Pred. No. 3.83e-63; Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps

DEFINITION ACCESSION NID KEYWORDS SOURCE ORGANISM g155643) kappa light chain: light chain: monoclonal antibody. house mouse. Nus musculus Rukaryotas: mitochondrial eukaryotes: Metazoa; Chordata; Verrebritas Dutheria; Rodentia; Sciurognachi; Muridas; Murinae; MCMAEMSTI 974 bp RNA ROD 01-0CT-1996 M. musculus mRNA for monocional antibody MST2 light chain. X79906

REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS TITLE JOURNAL (bases 1 to 974)

FEATURES source Janon N.

(Inpublished
2 (Dases 1 to 974)
3 Janon N.

Direct Submission
10 (24-JN-1994) N. Janon, Commissariat a l'energie,
atomique, Diep Bat. 152 CEN Saclay, 91191 Gif/Tvette Cedex, FRANCE
10 Continn Countifière
11 974
11 974
11 974
11 974

JOURNAL REFERENCE AUTHORS TITLE JOURNAL

o (bases 1 to 432) Naticle R. 8. Naticle R. 8. Naticle R. 8. Naticle Co. McV-1989 Daniels R.S., Virology Division, Mational Naticute for Mcdical Research, The Midgeway, Mill Hill, London, N7 1AA, UK

FEATURES Source

ocation/Qualifiers

/organism="Mus musculus"
/db\_xref="taxon:10090"
/rearranged
/cell\_type="hybridoms"
<1. >432

KEYWORDS SOURCE ORGANISM

lobulin; kappa chain; variable region

ACCESSION NID

REFERENCE AUTHORS

Nus missilus Bukaryota, Metasos, Chordata, Vertebrata, Mammalia, Eutheria, Bodantia, Seiucogpathi, Muridae, Murinae, Mus. 1 (Dasse 1 G. 437) Wrigley, M.G., Brown, E.B., Daniels, R.S., Douglas, A.R., Skehel, J.J. and Miley, D.C. (1nfluensa haemagglutinin-monoclonal antibot

microscopy of influenza haemagglutinin-monoclonal antibody

TITLE

RESULT 45
LOCUS
DEFINITION

557 432 bp mRRA, end ROD 11-NOV-1998 sculue mRRA for H3 epecific immunoglobulin, kappa chain, le region, partial.

CDS

/product\*iidht chain of the monoclonal antibody MST2'
/Ab\_xref\*PD1:e461939;
/Ab\_xref\*PD1:e461939;
/Ab\_xref\*PD1:e461959;
/Ab\_xref\*PD1:e461795FLISASYIMSRQQIVLYOSPAINSASLAERFYNT
CTASSSYNSSTLUHYOQDOSSPILMIYETSNIASGYPAFSGGGGCTSYSLIISNE
AEDALTYCHOTHEPPHTGGGTMLEIRAADAPTWSIFPPSSEDLISGGAFVGCTLN
MFTPGDIVMRIDGSERGGGVLISSWIDQDSKDSTTENSGTLIETURTETERHSYTCE
AFMINGSSPINSEC\* /product="light chain of the monoclonal antibody MST2" a 275 c 200 g 229 t ct="light chain of the monoclonal antibody MST2"
751

18.4%; Score 80; DB 29; Length 974

BASE COUNT ORIGIN

270 a

sig\_peptide V\_region

C\_region

Query Match

Apr 19 13:23:48

ORIGIN

ACCESSION U25101 g1002397

FEATURES Source Sgo /organism\*\*His musculus\*
/db\_xref\*\*taxon:10090\*
/cell\_line\*\*hybridoma cell line 7-4\*\*
<1-473 |

US-08-836-455-1.rge

KIYMORDS
SOURCE
AND SOURCE
SOU

2 (bases 1 to 473) 1.1
Emera, M.G., TOUT, N. 12; Kanabik, A. and Lam, J.S.
Direct Submission 1.2

Obery Match 18.2% Score 79: DB 29: Length 432;
Best Local Staffarity 100: Pred No. 5.25e-6;
Matches 79: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

RESULT 46
LOCUS
DEFINITION

NGU35101 473 bp. mRNA ROD 12-MAR-1996 Nus masculus anti-Peschomonas arruginosa inner core oligosaccharide of lipopolyeaccharide, ig light chain variable region mRNA, partial

note="MAb specific for inner core oligosaccharide of ipopolysaccharide of Pseudomonas deruginosa" codon\_start=1 Immunoglobulin 119ht chain" PID:g1002398" on="ELQNTQSPAINSASLGERVINTCTASSSYSSSYLHWYQQKPGSS

> M Sp Apr 19 13:23:48 1999

BASE COUNT

/product="immunoglobulin, kappa chain, variable region"
/db\_wref="PID:el]41344"
105 a 121 c 107 g 99 t

/note="monoclonal antibody Hc45" /codon\_start=1 /pseudo

/note="monoclonal antibody Hc45" product="immunoglobulin, kappa chain, wariable region" (1...)432

g V\_region

Page 75

US-08-836-455-1.rge

misc\_feature PKLWIYSTSNLASGVPARFSGSGSGTSYSLTISSMEAEDAATYSCHQYHRSPFTFGGG TKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERG"

J\_segment misc\_feature misc\_feature /note="enco-291. .324 /note="JK2" , 136 c 109 g 109 t /note=\*
151. .1
/note=\*
268. .2 incodes CDR2 encodes CDR1 ncodes CDR3\*

BASE COUNT ORIGIN Query Match 18.2%; Score 79; DB 29; Best Local Similarity 100.0%; Pred. No. 5.25e-62; Matches 79; Conservative 0; Mismatches C Length 473;

0; Indels 0; Gaps

RESULT 47
LOCUS
DEFINITION E03801 366 bp RNA PAT 26-NOV-1996
DNA sequence encoding a peptide which has a inhibition activity of binding ICAM-1 and LPA-1.

ACCESSION
NID
KEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS Hus sp. Hus sp. Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; g2172015 JP 1992193895-A/1.

Murine: Mus. 1 (Chaes 1 to 366) Akra.Y., Komo,I., Masayuki,T., Kumiko,H., Shinsuke,T., Junji,H. and Toshiaki,S.

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PACENT: 2P 1992193895-A 1 13-JUL-1992;

ANIKOMOPO CO INC

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PP 27-NOV-11990 JP 1990124763

PP 27-NOV-11990 JP 1990124763

PP 27-NOV-11990 JP 1990124763

PP 37-NOV-11990 JP 1990124763

PP 1 HAMPIN JNIK STAN, TSOUTSAKE MASAYUKE, HAMADA KUMIKO,

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                                                                                                                          ACCESSION
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Best Local Similarity 100 0%; Pred, No. 7, 16e-61;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps
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239 ANGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCGTTGAG 298
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CC strandeness: bouble;

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PM Key

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Eukaryotae: mitochondrial eukaryotes: Metazoa; Chordata;
Veriebrata; Eutheria; Modentia; Schurognathi; Myomorpha; Muridae;
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Kus museullus immunoglobulin kappa light chain variable region mRNA,
close MR2-169, partial cds.
U19326.
Nus sp.
Mus sp.
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                                                                                           869053 295 bp', mRNA ROD 22-8EP-1994 Ig V kappa wanti-p-nitrophenyl phosphonate esterolytic antibody kappa chain variable region [clone CNJ206] [mice, mRNA Partial, 869053 g545318
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Submitted (02-184-1995) Jessics H. Boark, Wister Institute, 3601
Spruce St., Philadelphia, PA 19104, USA
Location/Qualifiers
1. 261
1. 261
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1 (bases 1 to 246)

1 (bases 1 to 246)

Roark.J. F., Kuntz.C.L., Nguyen,K.A., Caton,A.J. and Erikson,J. Breakdown of B cell tolerance in a mouse model of systemic lupus erychematosus 11 tolerance in a mouse model of systemic lupus 5. Tapp. Red. 181 (3), 1157-1167 (1995)

2 (bases 1 to 246)
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J. Exp. Med. 181 (3), 1157-1167 (1995)
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Roark, J.H.
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/product*/peptide which has a inhibition activity of shiding ICAM-1 and LEA-1.
Location/Qualifiers
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DEFINITION Nummuneglobulin kappa light chain variable region mRNA,
ACCESSION U1917RL2-17, partial cds.

ROSSION U1917RL2-17 partial cds.
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Best Local Similarity 98.5%;
Matches 135; Conservative
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219 AMAGGTENGTGGGAGTAGGTCTGGGTCMGTTATTCTCTACCATCAGCAGCCGTGAGT 298
                                                                       1158 ALAMAGETTCAGTGGCAGTAGAGTTGGTGAGATTATTCTCTCACCATCAGCAGGCTTGAG 217
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                                                                                                                                                        GenBank staff at the Mational Library of Medicine created this entry [NCDI global 144395] from the original journal article. This sequence comes from Fig. 2.
Location/Qualifiers
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1 (bases 1 to 261)

Roark, J.H., Kuntt, C.L., Nguyen, K.A., Caton, A.J. and Erikson, J.

Breakdown of B cell tolerance in a mouse model of systemic lupus
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4 55 c 62 9 68 t
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/gene_19 Vakyr;
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SUMMARIES

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1:em\_est/2:em\_gss/4:em\_gss/3:em\_gss/3:em\_gss/3:em\_gss/3:embsn/emt/2:embsn/embs >US-08-836-455-1 (1-435) from USO8836455.seq 435 2275026 seqs, 895388244 بر 0 ATGGGGGCCCCTGCTCAGAT. Query 0 .CACCATCCAGTAAGCTTGGG n onit 435

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. F	Section   Sect	Mon Apr 19 13:23:50 1999 US-08-836-455-1.rst	15   3.4   467   8   MANORSSS   \$189701.11   Stratagene   1.26e+00   758   15   3.4   468   8   ALISPON   EST21491   Normalized   1.26e+00   758   15   3.4   468   8   ALISPON   EST21491   Normalized   1.26e+00   760   15   3.4   470   1   MASS240   vicilida.11   Normalized   1.26e+00   760   15   3.4   470   1   MASS240   vicilida.11   Normalized   1.26e+00   760   15   3.4   471   2   ANISPON   VICINIA   Homo appien   1.26e+00   760   15   3.4   471   2   ANISPON   WINDLE   Source   Required   1.26e+00   760   15   3.4   471   2   ANISPON   WINDLE   Source   Required   1.26e+00   760   15   3.4   471   2   ANISPON   WINDLE   Source   Required   1.26e+00   760   15   3.4   471   2   ANISPON   WINDLE   Source   Required   1.26e+00   760   15   3.4   471   2   ANISPON   WINDLE   Source   Required   1.26e+00   760   15   3.4   471   2   ANISPON   WINDLE   Source   Required   1.26e+00   760   15   3.4   471   2   ANISPON   WINDLE   Source   Required   1.26e+00   760   15   3.4   471   2   ANISPON   WINDLE   Source   Required   1.26e+00   760	Non Apr 19 13:23:50 1999 US-08-836-455-1.rat
		Page 19	·	Page 17
	\$10 15 3.4 589 6 AA121492 abb8alo.si Source preg 1.26+00 coll	Page 19 Hon Apr 19 13:23:50 1999 US-08-836-455-1.zet	808 15 3.4 498 28 AGL87144 HS_3122_Bl_ANO_TY CTT 1.56=00 810 15 3.4 498 28 AGL87145 HS_3122_Bl_ANO_TY CTT 1.56=00 810 15 3.4 498 28 AGL8725 HYPERION CARPES PLEE 1.26=00 811 15 3.4 497 6 611499 HS_306_Bl_ANO_TY CTT 1.56=00 812 15 3.4 497 8 AGL8726 HS_306_Bl_ANO_TY CTT 1.56=00 813 15 3.4 497 8 AGL8726 HS_306_Bl_ANO_TY CTT 1.56=00 813 15 3.4 497 8 AGL8726 HS_306_Bl_ANO_TY CTT 1.56=00 813 15 3.4 497 8 AGL8726 HS_306_Bl_ANO_TY CTT 1.56=00 813 15 3.4 497 8 AGL8727 HS_306_Bl_ANO_TY CTT 1.56=00 813 15 3.4 497 8 AGL8727 HS_306_Bl_ANO_TY CTT 1.56=00 813 15 3.4 497 8 AGL8727 HS_306_Bl_ANO_TY CTT 1.56=00 814 15 3.4 497 8 AGL8727 HS_306_Bl_ANO_TY CTT 1.56=00 815 15 3.4 497 8 AGL8727 HS_306_Bl_ANO_TY	Page 17 Mon Apr 19 13:23:50 1999 US-08-036-455-1.zet

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## ALIGNMENTS

RESULT 1
LOCUS
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ACCESSION NID

AA717201 125 bp mRNA EST 29-DEC-1997 rp44807.11 Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone 1079316 5' similar to gb: X53329\_cdel IG KAPPA CHAIN V-I REKION (HUMAN); mRNA sequence.

AX117201
AX117201
AX17201

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RESULT 2
LOCUS
DEFINITION
ACCESSION
NID
                                                                                                                                        71 CAGGAACCAGATGGAACTATTAAACGCTGATCTACGCGACATCCAGTTTAG
171 CAGGAACCAGATGGAACTATTAAACGCCTGATCTACGCCCACATCAGTTTAG
172 CAGGAACCAGATGGAACTATTAAACGCCTGATCTAGGCCCACATCAGTTAGG
                               205 bp mRNA EST
T-cell lymphoma Homo sapiens cDNA 5' end
obulin kappa light chain, V region, mRNA s
                               21-APR-1997
d similar to
sequence.
                                                                                                                                        122
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REYWORDS SOURCE ORGANISM GE I (bases 1 to 205)

I (bases 1 to 205)

RS Manny, E.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

RS Manny, E.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

White, C.J., whee, M.R., Kirkness, E.F., Weinstock, K.G., Gocdyne, J.D.,

White, C.J., whee, M.R., Kirkness, E.F., Weinston, R.C., Wann, Rill, C.,

Clayron, A. Michael, R. R., Rondon, R.C., Wann, J.D.,

Fitgerand L.W., Fitchush, W.R., Fritchman, J.R., Gocdynsen, W.S.,

Clodek, A., Gerha, C.L., Hanna, M.C., Hedblon, E., Hibblap, E.J.,

Kelley, J.M., Kelley, J.C., Liu, L.T., Marmares, S.M., Merrick, J.M.,

Koreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligino, S.M.,

Koreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligino, S.M.,

Koreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligino, S.M.,

Shall, K.V., Spriggs, T.A., Utterback, R., Keldman, J.F., Li, Y.,

Shall, K.V., Spriggs, T.A., Utterback, R., Keldman, T.A., Collins, E.J.,

Back, R., Hand, D., Cao, L., Cepeda, M.A., Colmen, T.A., Collins, E.J.,

Back, R., Hand, S., Geren, J.M., Colmen, T.A., Kalasher, P.S., Oleen, H.,

Back, R., Hand, S., Geren, J.M., Colmen, T.A., Collen, R.,

Back, R., Hand, S., Geren, J.M., Colley, J., Riddon, P., Kim, A.K.,

Back, R., Hand, S., Geren, J.M., Colley, J., Riddon, P., Kim, A.K.,

Back, R., Hand, S., Geren, J.M., Colley, J., Riddon, P., Kim, A.K.,

Back, R., Hand, R., Spriggs, R., Kim, R human. Romo sapiens Eukaryotae: mitochondriai eukaryotes: Metasos: Chordata: Vertebrata: Mammalia: Butheria: Primates: Catarrhini: Hominidae:

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FEATURES Source

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Location/Qualifiers
1. .205

Organisms"Homo sapiens"
//organisms"Homo sapiens"
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//organisms EcoRI; Site\_2

48 a

2 others

Query Match Best Local S Matches 4 ch 9.7%; t 1 Similarity 97.7%; F 42; Conservative Score 42; DB 25; Pred. No. 1.34e-60; 0; Mismatches 1 Length 205;

1; Indels

<u>..</u> Gaps

DEFINITION (15304,11 Barptead mouse irradiated colon MPLRB7 Mus musculius cDMA (1506,1507)
DEFINITION (15304,11 Barptead mouse irradiated colon MPLRB7 Mus musculius cDMA (1506,1507)
PURDION (15766,1507)
PURDION (15766,1

Zukaryotæ: Metasoa; Chordera; Yertebrata; Marmalia; Butheria;
Rodentia; Schurgnathi; Muridae; Murinae; Nus
( bases 1 to 35)
Marra, M., Hillieri., Allen, M., Bowles, M., Districh, M., Dubuque, T.,
Gelsei, S., Rucaba, T., Lacy, M., La, M., Martin, J., Mooria, M.,
Schelienberg, M., Steptee, M., Tan, F., Underwood, T., Moore, B.,
Thisisip, B., Wylie, T., Lenon, G., Soares, B., Wilson, R. and
Materiaton B., Wylie, T., Lenon, G., Soares, B., Wilson, R. and
Materiaton B., Wylie, T., Lenon, G., Soares, B., Wilson, R. and

Schellenberg, K., Steptoe, M., Tan Theising, B., Wylle, T., Lennon, G. Waterston, R. The WashU-HHMI Mouse EST Project Unpublished (1996)

Contact: Marra MyBouse BST Project
Weabli-HBMI House BST Project
Weabli-HBMI FOR BY PROJECT
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Par: 314 286 1800

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Page 21

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Page 22

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KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

/octawivetor P777DD-Des (Pharmacia) with a modified polylinker Site\_1. ECORI: Site\_2. RRIT; six awolding polylinker Site\_1. ECORI: Site\_2. RRIT; six awolding from 8 week old mouse. Colon was harvested? houseafter irradiation with 1400 Gys. Lat extend cDNA was primed with a Not I - oligo(d7) primer. Six awolding the Six awolding to the CORI and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library conservated by Bob Barstead. Six awolding the Six aw /organism="Mus musculus" /strain="PVB/N"

34

Query Match 12.0%; Best Local Similarity 100.0%; Matches 52; Conservative Score 52; DB 11; Length 125; Pred. No. 2.45e+87; 0; Mismatches 0; Indels 0; Gaps

ORGANISM

of normalisation to a Cot = 20. Library constructed by Bento Soares and M.Fatina Bonaldo.

Homo saplens
Eukaryotae: Metasoa: Eumetasoa: Bilateria: Coelomata:

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REPRODUS

human paimer-will Reverse library-Ruman Pancreas.

human paimer-will Reverse library-Ruman Pancreas.

Butteris, Goeloomate, Butteris, Goeloomate, Goeloomate, Butteris, Goeloomate, Goeloomate, Butteris, Children, Goeloomate, Goeloomate, Goeloomate, Butteris, Children, Goeloomate, Teresport, Annaber Cararbini, Hominidae, Homo.

Butheris, Archonta, Primates, Catarbini, Hominidae, Homo.

REFERENCE 1 (Dase 1 to 289)

Bult-C.J., Lee, N. Kirhess, E., Reinstock, K.G., Goeyne, J.D., white, O., Sutton, G., Likhess, E., Reinstock, K.G., Goeyne, J.D., white, O., Sutton, G., Banka, M. E., Brandon, R.C., Chiu, M. -W., FitzBugh, W. K., Fritchman, J. L., Geophagen, N. S. K., FitzBerald, L. M., FitzBugh, W. K., Fritchman, J. T., Marmaros, S. M., FitzBugh, J. K., K. Kelley, J. C., Liu, L. T., Marmaros, S. M., Ferrick, J. M., Sorien-Palanques, R. F., McDonald, L. A., Wyven, D. T., Ferrick, J. M., Stirey, R. Saalik, D. W., Socht, J. C., Liu, L. T., Marmaros, S. M., Felley, J. M., Stirey, R. Saalik, D. W., Stochad, L. A., Wyder, S. E., Soott, J. L., L., Fellem, J. M., C., Liu, L. J., Marmaros, S. M., Fellem, J. M., Stirey, R. Saalik, D. W., Cao, L., Cephagen, M. A., Fellem, J. M., Stirey, R. Saalik, D. W., Cao, L., Cephagen, M. A., Fellem, J. M., Stirey, R. Saalik, D. W., Cao, L. Wyen, D. T., Ferrick, M., Stirey, R. Saalik, D. W., Cao, L. W., Cephagen, M. A., Fellem, J. M., Charles, R. J. M., C., Waller, J. W., Carles, M., Stirey, R. Saalik, D. W., Cao, L. W., Cephagen, M. A., Fellem, J. W., Carles, M., Stirey, R. Saalik, D. W., Cao, L. W., Cephagen, M. A., Fellem, J. W., Carles, M., Stirey, R. Saalik, D. W., Cao, L., Cephagen, M. A., Fellem, J. W., Carles, M., Stirey, R. Saalik, D. W., Cao, L. W., Cephagen, M. A., Fellem, J. W., Carles, M., Stirey, R. Saalik, D. W., Cao, L. W., Cephagen, M. S. W., Carles, W., Carles, M., Carles, W., Carles, M., Carles, M.,
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                                                                                                                                                                                                                                                                            Overy Match 9, 19 15; Length 288; Best Local Similarity 100 01, Fred No. 2 56-50; Matches 38; Conservative ...0; Mismatches 0; Indels 0;
                                                                                                                          46 CCACATGTGACATCCAGATGACCCAGTCTCCATCCTCC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H24990 64 bp mRRA clone 160635 5' similar to gb:x00965_cdal IG KAPPA CHAIN PRECURSOR V-I REGION (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:632678
Seq primer: -30ml3 rev2 ET from Amersham
High quality sequence stop: 140.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Venter, JC
The Institute for Genomic Research
932 Cipper Rd, Gaitheraburg, MD 20878
932 Cipper Rd, Gaitheraburg, MD 20878
Fax: 3018899422
Fax: 3018899422
Fax: 1018699422
For clone availability, additional sequence and expression information related to this EST, please contact the TICR Database (tbb.focetdb.tipr.org)
105 Location/Qualifiers
1 . 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
<1. .>288 .
66 a 81 c | .71 g 67 t
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AUTHORS
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AUTHORS
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Best Local Similarity 88.4%; pred. No. 2.65e-50;
Matches 38; Conservative 0; Miamatches 5; Indels
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12 (Amers 1 to 197)

13 Addmin, H.D., Kerlavege, A.R., Pleischmann, R.D., Fuldner, R.A., B., Addmin, H.D., Kerlavege, A.R., Bandon, K.C., Moccyre, J.D., Bultic, O., See, N. H., Kirkness, E.P., Medinsko, K.G., Googyee, J.D., Chyleron, R.A., Clantha, B. Standon, K.C., Minness, M. S., Chyleron, R.A., Clantha, K.C., Thomas, M., Standon, R. S., Standon, R. S., Cologe, A. G., Chilli, M. K., Chyleron, R. S., Googyee, D. S., Cologe, A., G., Chilli, M. S., Chyleron, R. S., Medinsk, D.M., Shirley, R., Kelley, J.M., Ke
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EST100107 Roco sapiens clouk 5' end similar to immunoglobulin kappa
light chain gene V(I) region (HT:3862).
777581 chain gene V(I) region (HT:3862)
7/12 Decause.
Fal: 3018699056
Fax: 3018699423
Email: arkeriavetig:.org
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EST14475 Testis tumor Homo sapiens cDNA 5' end similar to immunoglobulin Kappa 11ght chair, V region, mRNA sequence.
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This close is available royalty-free through LLML: contact the This close is available royalty-lini.gov) for further information. Trace considered overall poor quality.
Location/Qualifiers
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The WashU Merck EST Project Unpublished (1995)
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Contact: Kerlavage, AR
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WashIngton University School of Medicine
WashIngton University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 285 1800
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Eukaryotae: hitochondrial eukaryotes: Hetazoa: Chordata;
Vertebrata; Mammalia; Eutheria: Primates: Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Institute for Genomic Research MD 20850 US
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Page 28

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Initial sassment of human gene diversity and expression patterns based upon 83 million nucleatides of CDNA sequence 977 (6547 Suppl), 3-174 (1995) 6026280 CREPERS (SUPPL), 3-174 (1995) C

e for Genomic Research Center Drive, Rockville, MD 20850

Email: arkerlayttygr.org | Email: Email:

Corganians-Momo septems'
/rotes'Organ: small intestine; Vector: pBluescript SK-;
/bb\_wret-NTCC (inhost):181667\*
/db\_wret-wrCC (inhost):181667\*
/db\_wret-wrC

8.7%; Score 38; DB 25; Length 301; Similarity 100.0%; Pred. No. 2.65e-50; Conservative 0; Hismatches 0; Indels 0;

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KEYNORDS ÉST.

SOURCEZ human.

ORGANISH Homo sapiena

Eukaryotas; mitochondrial eukaryotes; Hatazoa; Chordata; indicator de l'externation de l'extern
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Overy Match 97%; Score 99; DB 94; Length 352; Best Local Similarity 100 0%; Pred No. 2 58-50; Matches 38; Conservative 0; Mismatches 0; Indels 0;
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white, O., Sutta, M. B., Kikness, B. F., Weinstock, K. G., Goozane, J. D.,
white, O., Sutta, M. B., Kikness, B. F., Weinstock, K. G., Goozane, J. D.,
white, O., Sutta, M. B., Kolland, B., Brandon, R. G., Kan Wall, T., L.,
Fitzgerald, L. M., Fitching, M. B., Brandon, B. M., Holley, J. G., Golder, A., Gorber, C. L. Hann, M. C., Hedbland, J. J., Goodane, S. G., Hann, M. C., Hedbland, J. J., Goodane, G. M., Roberald, L. M., Byttep, D. T., Belley, J. M., Kelley, J. C., Liu L. J. Hannaros, M. M., Fitzley, S. M.,
Phillips, C. A., Ryder, S. E., Scott, J. L., Saudek, D. M., Shirley, S. M.,
Phillips, C. A., Weter, S. E., Scott, J. L., Saudek, D. M., Shirley, S. M.,
Fidharik, D. P., Coo, L., Cepeda, M. A., Colean, T. A., Colling, E. J.,
Sinke, D., Feng, D. F., Ferria, A., Fischer, C., Bastings C. A.,
He, W. H., Bu, J. S., Greene, J. M., Collean, T. A., He, M., S., Olsen, R.,
Raymond, L., Kai, Y. F., Wing, J., Xu, C., Yu, G. L., Ruben, S. M.,
Raymond, L., Kai, Y. F., Wing, J., Xu, C., Yu, G. L., Ruben, S. M.,
Raymond, L., Kai, Y. F., Wing, J., Xu, C., Yu, G. L., Ruben, S. M.,
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Raymond, L., Kai, Y. F., Wing, J., J., Yu, G., Yu, G. L., Ruben, S. M.,
Raymond, L., Kai, Y. F., Wing, J., J., Yu, G. J., Yu, G. L., Ruben, S. M.,
Raymond, L., Kai, Y. F., Wing, J., J., Yu, G., Yu, G. L., Ruben, S. M.,
Raymond, L., Kai, Y. F., Wing, J., J., Yu, G., Yu, G. L., Ruben, S. M.,
Raymond, L., Kai, Y. F., Wing, J., J., Yu, G., Yu, G. L., Ruben, S. M.,
Raymond, L., Kai, Y. F., Wing, J., Yu, G., Yu, G. L., Rub
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Bullt, C.J., Lee, H. H., Standbrann, R.D., Fuldner, R.A.,

Bullt, C.J., Lee, H. H., Standbrand, R.D., M.C., Kockyne, J.D.,

White, O., Sutton, G., Bake, J.B., Mediano, K.C., Robert, F.D.,

Clayton, R.A., Clibe, T.R., Octon, H.D., Octon, H.D.,

Firegerad, H.M., Fithens, M.C., Redblam, E., Mindeysen, J.F.,

Kelley, J.M., Kelley, J.C., Liu, L.T., Manners, S.M., Merrick, J.M.,

Kocteo, Palanques, R.F., McDonald, L.A., Sglyen, D.T., Pelligrin, S.M.,

Horeto, A., Nyders, E.E., Scott, J.L., Sudder, D.M., Shriey, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Liy, R.,

Bednarik, D.D., Coo, L., Cepeda, M.A., Colemn, T.A., Colling, E.J.,

Dinke, D., Fengo, D.-F., Ferris, A., Flesher, C., Rattings, G.A.,

Korak, D.L., Kunsch, C., Rungjun, J., Li, H., Meissner, P.S., Olsen, H.,

Korak, D.L., Kunsch, C., Rung, J., M.C., Yu, G.L., Ruben, S.M.,

Billion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, N.A., Fields, C.,

Fraser, C.M., and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mail: arkerlay@tigr.org
For chome availability, additional sequence and expression
information related to this EST, please check the Tigr Human Gene
index (http://www.tigr.org/tdb/hgi/hgi.html)
seq primer; hij Revorse.
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/Bote="Organ: testis: Vector: pBluescript SK-; Site_1: Nbc1:
/Ab_ref="Arco. those::191662"
/Ab_ref="Arco. 1906
/Gione_1ib="Testis tumor"
/dev_grage="adul-"
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Medical Center Drive, Rockville, MD 20850 USA
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/note "Organ; testis Vector: pBluescript SK-; Site_1:

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KEWHORDS ÉST.

ONGANTSH Homo appiens

OKGANTSH Homo appiens

Eukaryotas; mitochondrial eukaryotes; Hetazoa; Chordata;

Eukaryotas; Mammalia; Butheria: Primates; Catarrhini; Hominidae;

Vertebrata; Mammalia; Mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9

AA361497 157 bp mRNA EST 21-APR-1997

DEFINITION EST71040 T-cell lymphona Homo sapiens cDRN 5' end similar to

ACCESSION A561497

RID 9201052

KEYMORDS EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8

AAJO1251
BOCUS TABLE 153 bp mRNA EST 18-APR-1997
DEFINITION ESTIA181 Testis tumor Bomo sapiens cDNA 5' end similar to
ACCESSION ASO1261
NID 91851592
KEYNORDS EST.

KEYNORDS SET.

NIMMAN SET.
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NID
KEYWORDS
SOURCE
ORGANISM
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MEDLINE
COMMENT
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source
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Best Local S
Matches 3
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human. Romo sapiens Bukaryotae: mitochondrial eukaryotas: Metaroa: Chordata: Verrebrata: Mammalia; Butheria: Primates: Catarrhini: Hominidae:

Page

32

Gaps

Sioinformatics
The Institute for Genomic Research
The Institute for Genomic Research
Trai 101865912
Trai 101865912
Small arkerlayed
Small arkerlayed
To Additional sequence and expression
Information related to this EST, please check the TIOR Human Gene
Index (http://www.tigr.org/fdb/hgi/hgi/hgi/html)
Seq primer: Mil Reverse.

Homo.

(Amess 1 to 357)

(Amm, M. D., Karlavage, A.R., Pleischmann, R. D., Fuldner, R.A.,

Adama, M. D., Karlavage, A.R., Pleischmann, R. D., Wan-Kai, C.,

Bilt, C.J., Lee, M. H., Kirkness, E.F., Weinstock, K. G., Goosyne, J. D.,

Wilte, O., Sutton, G., Blake, J. A., Brandon, R. C., Man-Kai, C.,

(Alayton, R.A., Cilme, T.R., Cotton, M. D., Earle-Hughes, J., Fine, L.D.,

Filayton, R.A., Cilme, T.R., Cotton, M. D., Earle-Hughes, J. Fine, L.D.,

Filayton, R.A., Cilme, T.R., Cotton, M. D., Brithe, P.S. J.,

Filayton, R.A., Cilme, T.R., Cotton, R. J., Geoghasen, N. S.,

Filayton, R. M., Fithney, M. M., Fritchman, J.L., Geoghasen, N. S.,

Filayton, R. M., Filayton, M. M., Filayton, S. M., Merrier, A.A., Pilayton, S. M.,

Ball, K.V., Spriges, T.A., Itechman, T.R., Marting, D. M., K.,

Bednarik, D. P., Goot, C., Cepded, M.A., Coleman, T. M., Marting, D. J.,

Dimke, D., Feng, D. F., Ferrie, A., Fischer, C., Harting, C.D., K. M.,

Bednarik, D. F., Kerrie, M., Fischer, C., Harting, C., M., K.,

Bednarik, D. F., Kerrie, M., Fischer, C., Harting, C., Fischer, M.,

Bednarik, D. F., Kerrie, A., Fischer, C., Harting, C., Fischer, M.,

Bednarik, D. F., Kerrie, A., Fischer, C., Harting, C., Fischer, S. M.,

Karoka, D. L., Kinsch, C., Hangin, J., Li, H., Heissner, P. S., Olsen, H.,

Billiton, P. J., Fannon, M. R., Rosen, C. A., Haseltine, W. A., Fields, C.,

Filtal, assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence

10012207 TRC15717

Contact: Kerlavsge, AR

M. Malter, M. S. Filtay, A. Filtaye, A.,

M. Malter, M. S. Filtaye, AR

M. Malter, M. S. Filtaye, AR

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13:23:50
1999

US-08-836-455-1.rst

Mon Apr 19 13:23:50 1999

Page 34

Mon Apr 19 13:23:50 1999 RESULT 10
LOCUS 18 A295786 382 bp mRNA EST 18-APR-1997
DEFINITION EST100987 Pancreas tumor I Homo sapiens cDNA 5' end similar to
similar to immunoglobulin Xappa light chain, V region (GB:L01279),
ACCESSION MRNA sequence.
A295786 193481211 BASE COUNT ORIGIN FEATURES Source RESULT 12 LOCUS R31204 Query Match 9.74; Score 38; DB 25; Length 357; Best Local Similarity 100.0%; Pred. No. 256e-50; Matches 38; Conservative 0; Mismatches 0; Indels 0; Ouery Match 8.7%; Score 38. DB 16; Length 393;
Best Local Similarity 100 0%; Pred, No. 2.56e-50;
Matches 38; Conservative: .0; Mismatches 0; Indels 0; HOMO

Mores 1 to 192)

Millor, Karlavge, A.R., Fleishmann, R.D., Fuldner, R.M., Gockyne, J.D., Bulton, C. Levin, R. H., Kirhnes, E.F., Weinstock, K.G., Gockyne, J.D., White, O., Sutton, G., Baker, J.M., Brandon, R.C., Men-Maid, C., Merker, R.M., Chine, T.R., Cotton, M.D., Earle-Suphes, J.F., Fitsgerald, M.K., Fitshman, M.C., Hedblom, E., Hinkhe, P.S.J., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkhe, P.S.J., Kelley, J.M., Kelley, J.C., Liu, L.T., Karanses, S.K., Herrick, J.H., Koreno-Palanques, R.F., HcDonald, L.A., Syuyen, D.T., Pelligino, S.H., Phillips, C.A., Kyders, E.F., Scott, J.L., Saudek, D.M., Shriey, R., Shalli, R.V., Sprigger, A., Utterhack, T.M., Reinn, J.F., Li, F., Shalli, R.V., Sprigger, A., Cepeda, M.A., Colemn, T.A., Collins, E.J., Detharth, D.P., Colo, L.C., Elegin, M.C., State, C.J., Marker, P.S., Soott, R.M., Marker, C.M., Marker, P.S., Soott, R.M., Raymond, L., Wei, T.F., Hing, W.J., Li, B., Wedenser, P.S., Sootten, B., Raymond, L., Wei, T.F., Ming, J.J., Xu, C., Yu, G.L., Ruben, S.H., Raymond, L., Wei, T.F., Ming, J.J., Xu, C., Yu, G.L., Ruben, S.H., The Institute for Genomic Research
932 Clapper Md. Gaitherabury, MD 20878
761. 3018699055
Fax: 301869905
Fax: 301869915
Fax: 3 Initial Assessment of Ruman Gene Diversity and Expression Patterns Based typo 52 Million Basepairs of CDNA Sequence Unpublished (1959) Other\_ESTs: TRC24356 Adams, M. D., Kerlavage, A. R., Fleischmann, R. D., Fuldner, R. A., D., Bult, C. J., Lee, N., Kirkness, E. F., Weinstook, K. G., Goosyne, J. D., White, O., Sutton, G., Blake, J. A., Pandon, R. C., Chiu, M. \*M., Willer, O., Strope, R. A., Cline, R. T., Cotton, M. D., Zarle-Highes, J., Fine, L. Pittsfeerald, L. M., Fitzshey, M. M., Feitchman, J. L., Googhagen, M. S. M. Glodek, A., Geeha, C. L., Hanna, M. C., Hedblom, E., Hinkle Jr. P. S. Biomo eaplana Bukaryotas; mitochondrial eukaryotas; Metazas; Chordata; Verrebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; /organisms\*Homo sapiens\*
<1. >393
41. >393
88 a. 113 c | 196 g 94 t pterygii: Choanata; Tetrapoda; Amniota; Mammalia; Theria; Fia; Archonta; Primates: Catarrhini; Hominidae; Homo. Location/Qualifiers
1. .357 451 bp EST 2 others

RESULT 11
LOCUS T2755
DEFINITION ESTIC LOCUS 277593 293 bp mRNA cend similar to 06 SEP-1995
DEFINITION ENTINOESS Rome aspleme GDNA 5' end similar to immunoglobulin kappa
ACCESSION 737593
NID 9508591 ENTINOESS ROME SEPTIMENT AND 9508591 ENTINOESS Query Match 978; Score 38; DB 24; Length 382;
Best Local Similarity 100 08; Pred. No. 256-50;
Matches 38; Conservative 0; Hismatches 0; Indels 0; Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseitine,W.A., Fields,C., Fraser,C.H. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995) The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 Tel: 3018699056 Contact: Kerlavage, AR clone availability, additional sequence and expression omation related to this EST, please check the TIGN Human Gene ex (http://www.tigr.org/tdb/hgi/hgi.html)
primer: MJ Reverse: /organiam="scome aspine"
/note="Organism=scome aspine"
/note="Organism=scome aspine"
/note="Organism=scome aspine"
/note="Income asp Location/Qualifiers

Mon Apr 19 13:23:50 1999

DEFINITION yh62a07.rl Homo sapiens cDNA clone 134292 5' similar to gb:x00965\_cds1 IG KAPPA CHAIN PRECURSOR V-I REGION (HUMAN);.

ACCESSION NID KEYWORDS SOURCE

humin clone=134292 library=Soares placenta Nb2HP vector=p7f71D (Pharmacia) with a modified polylinher host=PBHOB (ampicillin resistant) primer=MiJBPI Asticl=Nbc IT Resist=Doo RI Female placenta botained spirch (ampicillin resistant) primer (ampic

DDN was ligated to Eco RI adaptors (Pharmacia, digested with Net I and cloned into the Not I and Eco H sites of the modified pl7737 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatina Bonaldo.

Homo sapiens DioCaryotae; Metasoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Butteria; Proatis; Gatarrini; Hominidae; Bomo. Juberia; Proatis; Gatarrini; Hominidae; Bomo. Juberia; Proatis; Gatarrini; Hominidae; Bomo. J. Hartan, M., Klobbar, T., Eliston, K., Hartan, M., Kuobbar, Le, H. Cannon, G., Marra, H., Paranon, J., Hittini, Bohlfing, T., Soares H., Tan, P., Tervashis, Z., Materston, R., Williamson, A., Wohldmann, P. and Wilson, R., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R., Waterston, R., Williamson, A., Wohldmann, P. and

The WashU-Merck EST Project Unpublished (1995)

REFERENCE AUTHORS

ORGANISM

Gontatt: Wilson RK
WashD-Wertz EST Project
WashIngson University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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444 Forest Parkway, Box 8501, St. Louis, MO 63108
444 Forest Parkway, Box 8501, St. Louis, M

BASE COUNT ORIGIN /organism="Homo sapiens" /clone="134292" 99 a 110 c 117 g 116 t

Onery Match 8.7%; Score 36; DB 5; Length 451;
Best Local Similarity 100.0%; Pred. No. 2.565-50;
Matches 38; Conservative 0; Mismatches 0; Indels 0; 86 CCAGATGTGACATCCAGATGACCCAGTGTCCATCCTCC 123

Gaps

RESULT 13
LOCUS
DEFINITION ACCESSION NID

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Page 38

Gaps 0

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53 CCAGATGTGACATCCAGATGACCCAGTCTCCATCCTCC 90
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WashIndrox EST Project
WashIndrox Dilversity School of Medicine
4444 Forset Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email 14 286 1810
Email 14 286 18
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Homo sepiens
Eukaryotae: mitochondrial eukaryotes; Metagoa; Chordata;
Verrebrata: Mammalia; Butheria: Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA300491 182 bb mRRM.
EST13109 Testis tumor Remo expiens cDNA 5 end sinilar to
impunoglobulin kappa light chain, v region, mRNA sequence.
AA300491
EST1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: arkerlayetigr.org Email: arkerlayetigr.org clone availability. Additional sequence and expression information related to this EST, please check the TIGE Human Gene Index (http://www.tigr.org/cdb/hgi/hgi.html) seq primer: Hil Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-Merck EST Project Unpublished (1995)
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Choanata; Tetrapoda; Anniota; Mamalia; Theria; Butheria; Archonta; Primates; Catarrhin; Honisidae; Hono; Hillera; Catarr, Chark, N. Dhuque, T., Elliston, K., Hawkins, M., Kunba, T., Le, M., Lennon, G., Marra, M., Bracana, H., Harta, M., Kunba, T., Le, M., Lennon, G., Marra, M., Paressan, H., Marra, M., Robiting, T., Saates, M., Tan, F., and Terevakia; B., Maccasson, K., Williamon, A., Wohdmann, F., and Wilson, R., Saates, M., Tan, F., Saates, M., Saa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human colon=141957 library=Soares placents Mb2HP vector=p7771D (Pharmacia) with a modified polylinker host=SHLDES (empicililin resistant) princer=MIRDS saftzl=Not I saftzl=Not I saftzl=Not I obtained at birth (fift) term). let strand cDNN was primed with a Not I - oligo(7) primer IS not resistant princer(1) primer IS not I saftzl=Not I - oligo(7) primer IS not I saftzl=Not I - oligo(7) primer IS not I saftzl=Not I - oligo(8) primer IS not I - oligo(8) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R67559 516 bp mRNA EST 30-MAY-1995 yi42hli.rl Romo sapiens cDNA clone 141957 5' Similar to gb:x0065_cdsl IG KAPPA CHAIN PRECURSOR V-I REGION (HUMAN); .
                                             Chases I to 283)

Amas M.D. Kerlawsej A.R. Fleischmann.R.D., Phidner, R.A.,
Ilt. C.J., Lee, N.R., Mithens J.R., Renden, R.C., Man. 4000 pre. J.D.,
Istero, Sutton, C., Blake, J.R., Renden, R.C., Man. 4000 pre. J.D.,
Asyron, R.A., Cline, T.R., Cotton, M.D., Earle-Susphe, J., Pine, L.D.,
Ittgerald, J.M., Fitchingh, M.M., Fitchingh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Organiame*Romo sapiens*
/Organiame*Romo sapiens*
/Dote-*Organi colon: Vector: pBluescript SK-; Site_1:
/Dote-*Organi colon: Vector: pBluescript SK-; Site_1:
/Dote-*Dote-*Colon: Colon: 
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/clone="141957"
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la; Chordata; Vertebrata; Gnathostomata; C
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Pred. No. 8.95e-48;
0; Mismatches 0; Indels 0;
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LOCUS
DEFINITION 1
LOCUS MA327542 266 bp BRNA EST DEFINITION ESTBO974 Colon I Homo sapiens CDNA 5' end similar ACCESSION AM327542 CMAIn, V resion, mRNA sequence. NID 9199558
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NID
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Best Local Similarity 97.4%;
Matches 37; Conservative
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                                                                                                                                                                      Query Match 8.7%;
Best Local Similarity 100.0%;
Matches 38; Conservative
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Contact: Kerlavage, AR
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EST10844 Colon I Home septens cDNA 5: end similar to immunogiobulin Rappa 119ht chain, V(1) region (GB:M64855), mRNA sequence.
AA327497
EST. 2019-1943
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The Institute for Genomic Research
7912 Medical Center Drive, Rockville, MD 20850 USA
701: 3018899056
FAX: 3018899423
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12 Medical Center Drive, Rockville, MD 20850 USA
1: 301899056
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/note="logan; tests; Vector: pBluescript SK-; Site_1:
Ecosi; Site_1: Xhoi: Vector: pBluescript SK-; Site_1:
/db_xree_""pxtoc (inhost): 192443"
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/olone_lib="Testis tumor"
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67 a. 75 c. 72 g. 66 t. 2 others
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Jone avaliability, additional sequence and expression
mation related to this EST, please check the TICR Human Gene
(http://www.tigr.org/tdb/hgi/hgi.html)
**imag: Mij Revetee.**
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ntion/Qualifiers
282
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Pred. No. 8.95e-48;
0; Mismatches 1; Indels 0;
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Mon

Apr 19 13:23:50 1999

BASE COUNT ORIGIN

AUTHORS

ORGANISM

FEATURES source

RESULT 15
LOCUS
DEFINITION ACCESSION NID

20-APR-1997 to immunoglobulin

Caps

Query Match 8.5%; Best Local Similarity 100.0%; Matches 37; Conservative

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19
13:23:50
1999

KEYWORDS SOURCE ORGANISM

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Page 41

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Mon Apr 19 13:23:50 1999
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US-08-836-455-1.rat

Page 42

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RESULT 18 A300788 303 bp. mRNA EST 18-APR-1997
DEFINITION EST11648 Testia tumor Homo sapiens cDNA 5 end similar to
ACCESSION A300788
NID 1253110
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Best Local Similarity 100.0%;
Matches 37; Conservative
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human
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Eukaryotes; mitochondrial eukaryotes; Netazoa; Chordata;
Vertebrata; Mammaila; Eutheria; Prinates; Catarrinni; Hominidae;
Vertebrata; Mammaila; Eutheria; Prinates; Catarrinni; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
Homo sapiens
Eukaryotae: mitochondrial eukaryotes; Metagoa; Chordata;
Verrebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo
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Bax: 30188994284517 org
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The Indictute for Genomic Research
797.2 Medical Center Drive, Rockville, MD 20890 USA
7el: 1018899923
Email: arkenizetigg: org
Email: arkenizetigg: org
Information related to this EST, please check the TigR Human Gene
Index (http://www.tigg.org/cdb/hgi/hgi.html)
Seq Primer: MI Reverse
Location/Omalifiers
1. 1886 Effortsonication
"(bases 1 to 303)
"Manna M.D. Kerlawers A.R., Pleischmann, R.D., Puldner, R.A.,
"Manna M.D., Kerlawers A.R., Pleischmann, R.D., Puldner, R.A.,
"Mike, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Mai, C.,
"Layron, R.A., Cline, T.R., Cotton, M.D., Barle-Hughes, J., Fine, L.D.,
"Elegerald, L.M., Fitchingh, M.K., Fritchman, J.L., Googhagen, N.S.,
"Clodek, A., Gnehm, C.L., Hanna, M.C., Hadblen, E., Hinkle, P.S.JT.,
"Kelley, J.M., Kelley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M.,
"Kelley, J.M., Kelley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M.,
"McCremo-Palanques, R.F., McDonald, L.A., Negyen, D.T., Selligrino, S.M.,
"Phillips, C.A., Negyer, S.E., Socret, J.L., Saudek, D.M., Shirley, R.,
"Phillips, C.A., Negyer, S.E., Socret, J.L., Saudek, D.M., Shirley, R.,
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Contact: Kerlavage, AR
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// Octaniam="Romo sep
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/motes Organ; oxlon; Vector: pBluescript SK-; Site_l:
EcoRI; Site_l: Xho!
/db_xref-"Nato (inhost):128302"
/db_xref-"taxon:9806"
/clone_lib="colon I"
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Kon

FEATURES Source

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RESULT 17
LOCUS 17
LOCUS 2765401 103 bp mRNA EST 21-APR-1997
DEFINITION EST65401 Lymph node, subtracted Romo sapiens cDNA 5 end similar to imminoglobulin kappa 119ht chain, V region (GB:D01279),
ACCESSION BASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
NID
KEYWORDS
SOURCE
ORGANISM
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Best Local Similarity 97.4%;
Matches 37; Conservative
                                                                                                                                                                                                                                   Admin.M.D. Kerlawig, A. M., Fleischmann, R.D., Fuldner, R.A., Bult.C.J., Lees. H. H., Kirkness, E. F., Meinsteck, K.G., Goosyne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wal, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hubbes, J.F., Fine, L.D., Fliegerald, L.M., Fitchman, J.L., Geophagen, N.S., Glodek, A., Gachm, C.L., Hanna, M.C., Redbons, E. Hinkle, P.S. J., Kelley, J.H., Kelley, J.C., Liu, L.-I., Marmaros, S. M., Merrich, S.M., Koreno-balanques, R.F., McDonald, L.A., Buyen, D.T., Pelligrino, S.M., Moreno-balanques, R.F., McDonald, L.A., Buyen, D.T., Pelligrino, S.M., Sadek, D.H., Shifey, R.M., Fine, J.M., Charley, J.C., McDonald, L.A., Buyen, D.T., Fright, A., Sadek, D.H., Shifey, R.M., Sadek, D.H., Shifey, R.M., Frieder, J.M., Frieder, J.M., States, C.M., Ramen, C.M., Sadek, D.L., Kunsch, C., Hungjun, J., L.H., Meismer, P.S., Olsen, H., Rozak, D.L., Kunsch, C., Hungjun, J., L.H., Meismer, P.S., Olsen, H., Rayrond, L., Wei, T.F., Mig, J., W.C., Tu, G.L., Ruben, S.M., Shifey, J.M., Shife, M.M., Shife, J.M., Shife
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryotae; miochondrial eukaryotes; Metaroa; Chordata;
Yertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37: DB 24; Length 286;
Pred. No. 8.95e-48;
0; Mismatches 1; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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Page 43

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Dillion, P.J., Pannon, M.R., Rosen, C.A., Haseltine, N.A., Fields, C..., Fraest, C.M. and Venter, J.C. Titiki, assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Mature 37 (6547 Suppl), 3-174 (1995) 90026200 TRC167177 198.7 A. Utterback, 7.R., Waldmin, J.F., Li.T.,
JOL. Gereda, M. Colemn T. A. Collis, E.J.,
7. Partie, M. Colemn T. A. Collis, R.J.,
Greens, J. M. Guber, J. Middon, P. Kin, M. K.,
Greens, J. M. Gruber, J. Middon, P. Kin, M. K.,
C. P., Wing, J. W. L. H. Halaner, P. S., Olsen, H.,
C. Wing, J. W. C. Yu, C. L., Ruben, S. M.
C. Wing, J. W. C. Willer, Ruben, S. M.
Collis, Rober, C.A., Maseitine, M.A., Fields, C.,
Collis, R. Rosen, C.A., Maseitine, M.A., Fields, C.,

The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 US ontact: Kerlavage, AR

MRNA BASE COUNT ORIGIN

KEYWORDS SOURCE ORGANISM

Email: arkerlavetigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdh/hgi/hgi.html)
Seq primer: Hi Reverse.

lon/Qualifiers

FEATURES source

/dev\_stage="adult" <1. >303 88 c 72 q Organism\* Romo sapiens\*
//octe\* Organism\* Romo sapiens\*
//octe\* Organis Realis / Voctor: pBluescript SK.; Site\_1:
ScoRi; Site\_1: Xho!
//db\_ref\*\*\*Organis (cinbes):192224\*
//db\_ref\*\*\*Cabon: 5006\*
//cbore\_lib=\*Testis cumor

Ouery Match 8 58, Score 37, DB 24; Length 303 Best Local Similarity 97.4% Pred. No. 8, 95e.48, Matches 37; Conservative 0; Mismatches 1; Indels 72 g 72 t Length 303; 2 others

o, Gaps

REGULT 18.3100891 303 bp mRNA EST 18-APR-1997 DEFINITION EST1001 Testia tumor Homo sapiena cDNA 5' end similar to immunoglobulin kappa light chain, V region, mRNA sequence.

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19
13:23:50 I
999

ACCESSION
NID
KEYWORDS
SOURCE
ORGANISM

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;

ESTs: THC167177 t: Kerlavage, AR

titute for Genomic Research dical Center Drive, Rockville, MD 20850 USA

Retlaytigr org

a wailability additional sequence and expression

ton relaced to this EST, please check the TICR Human Gene

tip://www.tigr.org/rdb/hgi/hgi.html)

ir: Mil Revetse.

Location/Qualifiers

1 303

Organism\*Homo sapiens\*
/Actor: PBluescript SK-; Site\_1:
/Boter\* Organ; testis; Vector: pBluescript SK-; Site\_1:
/Boter\* Organ; testis; Violation of California of Californ

Apr 19 13:23:50 1999

BASE COUNT ORIGIN /organism="Homo sapiens" /clone="152681" 74 a 92 c 83 g 85 t

1 others

0

Homes to 203)

1 (bases to 203)

Adams, M.D., Kerlavage, R.F., Wainstock, K.G., Goosane, J.D., Bult.C.J., Lee.N.H., Kirkness, E.F., Wainstock, K.G., Goosane, J.D., Bult.C.J., Lee.N.H., Kirkness, E.F., Wainstock, K.G., Goosane, J.D., Bult.C.J., Lee.N.H., Kirkness, E.F., Wainstock, K.G., Goosane, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man. Hall, C.G., Clayton, R.A., Cliner, R., Cotton, M.D., Ezric-Haghes, J.F., Fise, L.D., Fitzgerald, L.M., Fitzhush, W.F., Fischesn, J.H., Googhagen, N.S., Glodek, N., Goehn, C.J., Hanna, M.C., Hedblom, E., Hitze, P.S. J.F., Kelley, J.H., Kalley, J.C., Liu, L.T., Marmaros, S.M., Merrick, J.M., Kelley, J.H., Kalley, J.H., L.M., Kelley, J.H., Morrio, B.H., Martick, D.H., Kelley, J.F., J., Scott, J.L., Saudek, D.H., Shitzley, R., Scott, J.L., Saudek, D.H., Shitzley, R., Scott, J.L., Saudek, D.H., Shitzley, R., Martick, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collin, E.J., Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, C.A., Kozak, D.L., Kussch, C., Hungjun, J.L.H.H., Melsaner, P.S., Olsen, H., Raymond, L., Wel, Y.F., Wang, J.T., Xu, C.L., Ruben, S.M., Dillion, P.J., Fannon, K.R., Rosen, C.A., Hasseltine, W.A., Fielde, C., Dillion, P.J., Fannon, M.R., Rosen, C.A., Hasseltine, W.A., Fielde, C., Dillion, P.J., Fannon, M.R., Rosen, C.A., Hasseltine, W.A., Fielde, C.,

Email: estewateon wustl.edu
High quality sequence stops: 235
Source: MAGE Consortium, LENU
This clone is available royalty-free through LENU; contact the
IMAGE Consortium (infostmange.linl.gov) for further information.
Location/Qualifiers
1. .135

Ouery Match 7,8%; Score 34; DB 5; Length 335; Best Local Similarity 100.0%; Peed. No. 2,61e-40; Matches 0; Indels

RESULT 21 LOCUS DEFINITION AA29542 203 bp mRM EST 2018, F. 197 EST100796 Pancreas tumor I Homo sapiens CDNA 5 end similar to immunoglobulin kappa light chain, V region, mRNA sequence.

ACCESSION AA290xxx
g194997
REPRORES
EST.
SOURCE
NUMBO sapiens
ORGANISH Homo sapiens
EMARYPOTES: Extraction: Chordata; Entheria; Potes: Metazoa; Chordata; Hominidae;
Verrebrata; Mammalia; Entheria; Potes: Metazoa; Chordata; Hominidae;
Verrebrata; Mammalia; Entheria; Potes: Metazoa; Chordata; Hominidae;
Verrebrata; Mammalia; Entheria; Potes: Metazoa; Chordata; Maniatoo, K.G., Googaye, J.D.
Waniatoo, K.G., Googaye, J.D.
Waniatoo, K.G., Googaye, J.D.
Waniatoo, K.G., Googaye, J.D.
Waniatoo, K.G., Googaye, J.D.

Mon Apr 19 13:23:50 1999

Initial sassament of human gene diversity and expression patterns based upon 83 million nucleatides of CDMA sequence Meture 377 (6547 Suppl), 3-174 (1995) 6026280 other\_ESTs: TRIC(67177 Contact: Ketlawage, AR

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9712 Hedical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056

Tall 101669423

Baxi 101669423

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Baxi 101669423

Baxi 1016604

Information wellabed ty, and EST, please oheck the Tion Ruman Gene Index (http://www.tigr.org/rdb/ngi/ngi.huml)

Ged priner: All Bewerse org/rdb/ngi/ngi.huml

Ged priner: All Bewerse org/rdb/ngi.huml

Ged priner: All Bewerse org/rdb/ngi.huml

/organiem="Homo saplens"
/organ: pancress; Vector: pBluescript SK-; Site\_1:
/organ: pancress; Vector: pBluescript SK-; Site\_1:
/organ: Anco: (inhost):191063\*
/organity-farchess tumor I\*
/dev\_stage="adult"
/dev\_stage="adult

Query Match 7.6%; Best Local Similarity 97.1%; Matches 33; Conservative Score 33; DB 24; Length 203; Pred. No. 7.25e-38; 0; Mismatches 1; Indels 0;

RESULT 22
LOCUS AA29508 292 bp mRNA EST 18-APR-1997
DEFINITION ESTIGO751 Pancreas tumor I Romo sapiens cDNA 5' end similar to
Limunogidoulin kappa light chain, V region, mRNA sequence.
NID 91947914
KEYWORDS EST. 921947914
EXTYPORDS human.
ORGANISH Homo sapiens
ENEATYPORAS: micochondrial eukaryotes: Metazoa: Chordata:
Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Hominidae:

Mon Apr 19 13:23:50 1999

Page 45

US-08-836-455-1.rst

Page 46

/dev\_stage="adult" <1..>303 70 a 83 c 75 g

Query Match 8.3%; Score 36: DB 24: Length 303; Beat Local Similarity 94.7%; Pred No. 280e-45; Indels 0; Manatches 36: Conservative 0: Mismatches 2: Indels 0;

ACCESSION NID KEYWORDS SOURCE RESULT 20
LOCUS E
DEFINITION 1 R49881 335 bp mRNA CEST 18-MAY-1995 yl5500 r1 Homo ampiena cDNA clone 1526815' similar to 92-X00995\_cdal to MAPPA CHAIN PRECURSOR V-I REZION (HUMAN); . 848881 g611783

(Pharmacia) with modified polylinker bosterNiDB (ampicillin) resistant; primaryMJRP1 Reice Not : Reite Dost MR (100 ampicillin) let strand colm was primaryMJRP1 Reice Not : Reite DeBco RI Adult female. Int strand colm was primary with a Not : oligo(CT) primer [5] double stranded colm was ilgated to Bco RI adaptors (Pharmacia), disperted with Not I and closed into the Not I and Eco RI sites of modified primy vector (Pharmacia), Library won through one round concerned at Reicha Boaldo. 20. Library won through one round goarse and H. Reicha Boaldo. 20.

REFERENCE AUTHORS ORGANISM

Eukaryotes; Metasos; Eumetasos; Bilateris; Coelonats; Osteichthyes;
Deuterrostonis; Chordats; Vertebrata; Gnathostonats; Osteichthyes;
Barcopterygii; Choanats; Tetrapods; Amilots; Mammalia; Theris;
Eutheris; Accobats; Prinates; Getarrhin; Hookindes; Romo;
I (Dases 1 to 35)
Hillier, L. Clark, H., Dubuque T., Elliston, K., Havkins, M.,
Hillier, L., Clark, H., Dubuque T., Elliston, K., Havkins, M.,
Holman, M., Bultans, K., Kucabi, J., Le, M., Lemon, G., Marra, M.,
Paraens, J., Hilton, L., Robbing, T., Seares, H., Tan, P., and
Wilson, B., Waterston, R., Williamson, A., Wolldmann, P., and
Wilson, B., Waterston, R., Williamson, A., Wolldmann, P., and

The WashU-Merck EST Project Unpublished (1995)

Contact: Hilson RK Washinytherk EST Project Washington University School of Hedicine 4444 Forest Path Fariway, Box 8501, St. Louis, MO Tal: 314 286 1800 Fax: 314 286 1800

NO.

Apr 19 13:23:50 1999

53 CCAGATGTGACATCCAGATGACCCAGTCTCCA 84

RESULT 23 LOCUS DEFINITION

AA019712 530 bp mRNA EST 117-FEB-1998 UT-R-AO-ap-e-12-0-01.8 UT-R-AO Rattus noregicus cDNA clone UT-R-AO-ap-e-12-0-UT 3 similar to gb|H14434|BATICANB Rat ig active Rappa-chain mRNA VJC-region from immunocytoma IR2, mRNA sequence.

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RESULT 24
LOCUS
DEFINITION
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Best Local Similarity 96.9%;
Matches 31; Conservative
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Bill C. J. Ler, N. H. Kirkness E.F. Weinstock, G. Gocayne J.D., Bills C. J. Ler, N. H. Kirkness E.F. Weinstock, G. Gocayne J.D., White, O. Strion, G. Bake, J.A., Bendon, R.C. Wan-Walc, C. Gocayne, J.D., Claycon, R.A., Cline, T.R., Cotton, H.D., Earle-Hubbes, J. F. Fitzgerald, M.K., Fitshugh, H.M., Fritchman, J.L., Googlade, N.S., Cline, J.R., Cotton, H.D., Earle-Hubbes, J. F., Kolley, J. K., Kelley, J
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Kelley, J.M., Kelley, J.C., Liu, L.T., Manmares, M., Merrick, J.M.,
Moreso-Palanques, R.P., Medbonald, L.A., Neuven, D.P., Phillips, G.M.,
Moreso-Palanques, R.P., Medbonald, L.A., Neuven, D.P., Phillips, G.M.,
Phillips, C.A., Pyder, S.E., Scott, L.L., Suddki, D.M., Shirlay, R.,
Small, K.V., Serigag, T.A., Utterbock, T.R., Weidman, T.P., L.J.,
Bednarik, D.P., Cooptel, M.A., Cuchem, T.A., Collion, E.J.,
Bednarik, D.P., Cooptel, M.A., Cuchem, T.A., Collion, E.J.,
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Bonne, D.L., Kunsch, C., Pretis, A., Pischer, C., Middon, P.J., Rin, A.N.,
Kozak, D.L., Kunsch, C., Weither, J.M., Masentrip, S.M., Dillion, P.J., Pannon, M.R., Rosen, C.A., Hasentrip, S.M., Fields, C.,
Praeer, C.M., and Venter, J.C.

Initial assessment of human gene diversity and expression patterns
based upon 33 million nucleotides of CDNA sequence

Nature, 377 (5547 Suppl.), 3-174 (1955)

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Bomo appiema
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Verrebbata; Mammalla; Butheria: Primates; Catarrhini; Hominidae;
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EST77625 Pancreas tumor III Homo sapiens cibat S'
sinilar to immunogiobulin light chain, V region,
AA56685
Contact: Kerlavage, ÁR
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132 a 110 c 151 g 137 t
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sedical Center Drive, Rockville, MD 20850 USA
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e availability, additional sequence and expression
ton related to this EST, please check the TIGR Human
tip://www.tigr.org/tdb/hgi/hgi.html)
tr: Mil Reverse.
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Pred. No. 4.68e-33;
0: Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 g 67 t
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ORGANISM RESULT 25 LOCUS DEFINITION FEATURES source Cuery Match 6.4%; Score 28: DB 25; Length 281
Best Local Similarity 96.6%; Pred. No. 4.57e 25;
Matches 28; Conservative 0; Mismatches 1; Indels Komo.

Adams M.D., Kerlavege A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult.C.J., Lee, N.H., Kirkness E.F., Weinstock, K.G., Gocsyne, J.D.,
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Clayton, R.A., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fittgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
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For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Ruman Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M1 Reverse. 55 A Organizam\*Homo aspiena\*
/note\*\*Organ, pancreas; Vector; phluescript
Reall; 61c,2; Mod?\*
/db\_tref\*\*Arce (nihost):171320\*
/db\_tref\*\*Arcen 9606\*
/db\_tref\*\*Ar on/Qualifiers 76 g 66 t Length 281; 3 others 21-APR-1997 'end similar to A sequence. <u>..</u>

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8 Apr 19 13:23:50 1999

Page 53

BASE COUNT ORIGIN KEYWORDS ÉST.

KEYWORDS ÉST.

ORGANISH Homo sapiens

ORGANISH Homo sapiens

Eukaryotas; mitochondrial eukaryotes; ketasoa; chordata; ketasoa; chordata; ketasoa; chordata; vertebrata; kammalia; Eutheria; Primates; Catarrhini; Rominidae; Vertebrata; Rominidae; Vertebrata; Rominidae; Ro RESULT 27
LOCUS 27
LOCUS ESTILLED 195 bp mRNA EST 18-APR-1997
DEFINITION ESTILLED GLOVE : Lumbr I Homo aspiens CDNA 5' end similar to similar (0.8:LD3678), mRNA sequence.

ACCESSION AJ99376 , mRNA sequence.

RID 91951958 EST.

91951958 EST. Apr 19 13:23:50 199 Query Match 6.4%; Best Local Similarity 96.6%; Matches 28; Conservative ER (Ames 1 to 195)

12 (Ames 1 to 195)

13 (Ames 1 to 195)

14 (Ames 1 to 195)

15 (Ames 1 to 195)

16 (Ames 1 to 195)

16 (Ames 1 to 195)

17 (Ames 1 to 195)

18 (Am 63 CATCCAGATGACCCAGTCTCCATCCTCC Kelley,J.M., Relley,J.C., Liu,L.-I., Marmacos,S.M., Merrick,J.M.,
Phillipp.C.A., Ryder;S.E., McDonald,L.A., Ngureno-Pakanques,R.F., McDonald,L.A., Ngureno-Pakanques,R.F., McDonald,L.A., Ngureno-Pakandos,R., Phillipp.C.A., Ryder;S.E., Scott,J.L., Saudak,D.M., Phillipp.C.A., Shighton,S.M.,
Small,K.V., Springer, A., Uterbeck,T.R., Medham,J.F., Lid,Y.,
Small,K.D.F., Coo,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dillach,D., Ferrick,A., Guber,J., Haddman,J.F., Kim,A.K.,
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Necesk,D.L., Kunach,C., Rungiun,J., Li,H., Heissner,F.S., Olsen,H.,
Dilling,D.J., March, M., March, M., Li,H., Heissner,F.S., Olsen,H.,
Dilling,D.J., March, M., March, M., Kang, M., March, M., March bilinovation The Mind Research (Mind H25952 Contact: Kerlavage, AR Email: arkerlayetig;.org additional sequence and expression for clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/ngi/ngi.html) Seq primer: httl Reverse.

Seq primer: http://www.tigr.org/tdb/ngi/ngi.html) Location/Qualifiers
1. 288 /organiam="Rome aspiens"
/note="organ; puncteas; Vector; pBluescript SK-; Site\_1:
/note="organ; puncteas; vector; puncteas; ESTs: THC167177 t: Kerlavage, AR e for Genomic Research Center Drive, Rockville, ND 20850 USA 243 bp Score 28; DB 25; Length 288; Pred. No. 4.67e-26; 0; Mismatches 1; Indels 0; EST 10-JUL-1995 SORRE STATEMENT COORSELES INTERPREDICT STATEMENT STATEME Mon Apr 19 13:23:50 1999 NID ET.
KEPYODDS ST.
SOURCE DUBANTS Homo sapiens
ORGANISH Homo sapiens
Eukaryotas; mitochondrial eukaryotas; Metazoa; Chordata; Eukaryotas; Metazoa; Chordata; Eukaryotas; Metazoa; Chordata; Meminidas;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidas;
Vertebrata; Mammalia; Mammalia; Eutheria; Primates; Catarrhini; Hominidas;
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Admin. M. D., Krizhvaga, A. R., Fleischmann, R. D., Fuldner, R. A.,
Balins, M. D., Krizhvaga, A. R., Fleischmann, R. C., Man. Wal, C.,
Clayton, S. W. C., Santon, G. C., Man. Wal, C.,
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Moreno-Palanques, R. F., McDonald, L. A., Muyenob, R., Millipa, C. A.,
Phillipa, C. M., Ryder, S. G., Soctet, L. L., Saddeb, D. M., Shilly, M.,
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Bedmarkh, D. F., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, J.
He, W. Hu, J. S., Green, J. M., Gruber, J. Hastings, G.A.,
He, W. Hu, J. S., Green, J. M., Gruber, J. Hastings, G.A.,
Rosak, D. L., Kunech, C., Hungju, J., Li, H., Meisener, P. S., Oleen, H.
Raymond, L., Weil, Y. F., Wing, J., Xu, C., Yu, G. L., Ruben, S. M.,
Dillion, P. J., Fannon, M. R., Rosen, C. A., Haseltine, W. A., Fields, C., ANA01279 Testa tumor Romo saptens CDMA 57 end similar to immunoglobulin kappa light chain, V region, mRNA sequence. ANA01279 257. Contact: Wilson RK
WashD-Merck EST Project
WashIngton University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO
761: 114 285 880
Park 114 286 8810
Estation on wutl.edu ylisao7.rl Homo sapiens cDNA clone 162228 5' similar to gb:X00965\_cds1 IG KAPPA CHAIN PRECURSOR V-I RECTON (HUNAN);. H25952 995075 Enall: estwarten wietledu Banli: estwarten wietledu Banli: estwarten wietledu Banli en This clone is available royalty-free through LLML: contact the THAGE Consortium (infodiance llnl.gov) for further information. Location/Qualifiers Wilson,R.
The WashU-Merck EST Project Unpublished (1995) /organism="Homo sapiens" /clone="162228" 52 a 73 c 65 g 57 /organiam="Homo aspiens"
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Gaps

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Mon Apr 19 13:23:50 1999
                                                               REFERENCE
AUTHORS
1 (bases 1 to 237)
Sohn, D., Park, D.S., Lee, C.M.,
Hvang, M.Y. and Jin, S.W.
Hwang, M.Y. and Jin, S.W.
Human HTCDL1 library cDNAs
Unpublished (1994)
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Apr 19 13:23:50 1999 Guery Match 6.0%; Score 26: DB 24: Length 196; Best Local Similarity 92.9%; Pred No. 147e-21; Matches 26: Conservative 0: Mismatches 2; Indels 0; ORGANISM Contact: Milaon RK

WashDriberts MST Project
WashIngton University School of Medicine

444 Forcet Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Email: est@wateon.vustl.edu

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Information Polaced to this EST, please Check the TIGR Human Gene
Index (http://wlig.org/tcb/mg//mgl.html)

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Deutomatmia, Chordata, Vertebrata, Gnathoscanta, Ostacichthyes;
Saccoptengii; Chomanta, Tetrapoda, Amnicha, Mammalia Theria;
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Hillard, J., Charley, M., Lannon, G., Marra, M.,
Parsons, J., Ritin, L., Shohiding, T., Soares, M., Tan, F., and
Wilson, B., Watczeton, R., Williamson, A., Wohldmann, P. and 725787 10-MAR-1998 mRNA E27 10-MAR-1998 TROPE TO Immunoglobulin Kappa chain VK-1, mRNA sequence. 725787 2254784 EST. Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nuclectides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
90202380 NGOO sapiens Eukaryota; Metasoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidas; Homo. e WashU-Merck EST Project published (1995) 50 g 14 t US-08-836-455-1.rst 10 others 4 others 0 Gaps

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FEATURES source

Norea
Tel: 82-053-950-5382
Tel: 82-053-955-5317
Pax: 82-053-955-5317
Pax: 82-053-955-5317
Pax: 82-053-955-5317

Ext Lis putatively homologous to Immunoglobulin kappa chain (GenBank, M54855) in human with 88% (39/44) identity.

Seq primer: M13 Reverse/SR primer.

Location/Qualifiers

regariam\*\*Homo aspiens\*

ode\*\*Vector: phisescript cN(-); Site\_1: EcoNI: Site\_2:

code\*\*Vector: phisescript cN(-); Site\_1: EcoNI: Site\_2:

phisescript contains, EcoNI cloning in the vector

litescript (Strategene).

b\_refet\*\*Anon:9606\*

clone\_1lb\*\*MYCLOSIO\*

do. 57 g 62 t

Contact: Uik
Sohn D.S. Park, C. H. Lee, M. X. Cho, H. J. Ahn, M. Y. Lee, M. Y. Hwang, S. W. Jin
Laboratory of Molecular Biology
Kyungpook National Univ. Taegu 703-701,
Dept. of Genetic Eng., Kyungpook National Univ., Taegu 703-701,

B

RESULT 29 LOCUS DEFINITION ACCESSION

BASE COUNT ORIGIN

Overy Match 5.5%; Score 24: DB 16; Length 87; Best Local Similarity 88.9%; Prod. No. 3.19e-17. Matches 24: Conservative :0: Mismatches 3; Indels 

T27721

288

bp · mRNA

rs3

06-SEP-1995

ACCESSION NID DEFINITION EST13641 Homo sapiens cDNA 5' end similar to chain V region, rearranged (HT:3785). T27721

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KURAN Primer-MJ Reverse library-Ruman Testis.

ORCANISH Romo asplens

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Dikaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Oseichthyes;

Dikaryotae; Metazoa; Chonata; Tetrapoda; Amniota; Mammalia; Theria;

Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammaliae; Homo.

Eutheria; Archouta; Primates; Catarhini; Bominidae; Homo.

Entheria; Archouta; Oseichthyes; Catarhini; Bominidae; Homo.

Principal Archoris Primates Catarrhini; Hominidae; Homon Indee; Lobase 1 to 288)

Radams M.D., Kerlawage A.R., Plaischmann R.D., Fuldmerr R.A., Milter J., Lee N., Kithness E.F., Weinstock, K.G., Goosyne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, H. H., Pittigerald, I.K., Pitti

FEATURES source

BASE COUNT ORIGIN Query Match 5.5%; Score 24; DB 16; Length 288; Best Local Similarity 96.0%; Pred. No. 3.19e-17;

/organism="Homo sapiens"
<1. .>288
a. 75 c. 70 g. 61

70 g

67 t

Mon

Page 59

Apr 19 13:23:50 1999

H24602 87 bp mRNA clone 160685 5' similar to ph.70095\_cds1 IC MAPA CHAIN PRECURSOR V-I RECION (HUMAN);.
SOURCE human classes.

human clone=160685 library=Soares breast 3NbHBst vector=p7773D (Pharmacia) with a modified polylinker host-DHIOS (ampicillin resistant) primer=YMJRSI asitel=Not I asite=Eco RI Adult human last strand cDNA was primed with a Not I - oligo(dT) primer (5'

Query Match 5.7%; Score 35: DB 13: Length 237; Best Local Similarity 100 0%; Pred. No. 2 Ree-19; Matches 25: Conservative 0; Mismatches 0; Indels

Indels 0;

Matches

24: Conservative 0;

Mismatches

Gaps 0

RESULT 32
LOCUS
DEFINITION

AA29541 289 bp mRMA EST 16-ABP-1997
EST101050 Pencreae tumur I Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, V region, mRMA sequence.

AA26541

Page 62

ACCESSION AA295wa g1942177
REYMORDS EXT.
SOURCE human.
ORGANISH Homo sapiens
Chargotae: micochondrial eukaryotes: Metazos: Chordata, incheria; Puthates; Catarrhini; Hominidae; Verrebrata: Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pathates; Catarrhini; P

Homo.

I (base 1 to 289)

Adams.M.D., Realwage, A.R., Fleischmann, R.D., Fuldner, R.A., D., Adams.M.D., Realwage, A.R., Fleischmann, R.D., Fuldner, R.A., D., Adams.M.D., Reich, G., Gocayne, J.D., White, G., Sutton, G., Blake, J.A., Brandon, R.C., Man-Bai, C., Firegrein, R.A., Collier, T.R., Cotton, M.D., Exite-Huybea, J., Fine, L.D., Flegerid, L.M., Fleinugh, M.K., Fitchman, J.L., Geoghagen, M.S., Gladgerid, M. Geoghagen, M.S., Gladgerid, M. Geoghagen, M.S., Manna, M.C., Hebbons, J.R., Hinkle, P.S.J., Raidel, D.M., Manna, M.C., Hebbons, J.M., Manna, M.S., Heligrino, S.M., Marracos, S.M., Merrick, J.M., Moreov-Palaur, R.B., Mosch, C.L., Ruben, D.J., Palligrino, S.M., Moreov-Palaur, M. Gath, L.A., Naymon, J.M., Glilins, F.J., M., Moreov-Palaur, M. Geoghagen, M. Gath, J. J., L.T., Beddin, J.F., L.T., M. Green, J.M., Charlet, J.M., M. Gath, J.M., M. Green, J.M., Geoghagen, J.M., Callins, F.J., J.M., M. Green, J.M., Geoghagen, J.M., Callins, F.J., J.M., M. Green, J.M., Geoghagen, J.M., Callins, F.J., J.M., M. Green, J.M., Gladger, J.M., M. Gladger, J.M., M. Gladger, J.M., M. Gladger, J.M., M. Gladger, J.

Nature 377 (6547 Suppl), 96026280 Other\_ESTs: THC167177 Contact: Kerlavage, AR Bioinformatics

The Institute for Genomic Research 9712 Medical Center Drive, Rockville, Tel: 3018699056

MD 20850 US

rax. 30185942) Email: arkerlavetigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene

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Page 63
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                                                                                                                                                                                Ouery Match 5.1%; Score 22: DB 15; Length 166; Best Local Similarity 84.6%; Pred. No. 4.28-13; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
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Individual construction to a Cot = 20. Library constructed by Bento Sources and K. Fathma Bonaldo.

Richaryotae; Metasos; Eumetasos; Blateria; Coelomata; Coelo
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CE 1 (bases 1 to 413)

Adams M. D., Kelavage A. R., Fleischmann R. D., Fuldner R. A.,

RS Adams M. D., Lee N. H., Kirkness E. F., Weinstock R. G., Googye J. D.,

White O., Sutton G., Blake J. A., Brandon R. C., Man Wai C.,

Clayton R. A., Cliner T. R., Cotton M. D., Earle Hughes J., Fine, L. D.,

Fitigerald, L. M., Fitchush M. M., Fritchman J. L., Geoghagen N. S.,

Clodek, A., Gehm, C. L., Banna, M. C., Redbloom, F., Hahle, P. S. J.,

Kelley J. H., Kelley J. C., Liu L. T., Marmares S. M., Merrick J. M.,

Kerner, Falangues R. F., Mobonald, L. A., Wguer, D. T., Pelligrino S. M.,

Phillips, C. A., Ryder, S. E., Scott, J. L., Saudek, D. M., Shirley, R. M.,

Bednarth, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J.,

Dinke, D., Feng, D. F., Ferrie A., Fisher, C., Hastings, C. A.,

He, M. M., Hu, J. S., Greene, J. M., Gruber, J., Hudson, P., Kim, A. K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The control of the co
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AAJO11479 Testia tumor Romo eaptens cDNA 5: end similar to similar
to immunoglobulin kappa light chain, V region (Gi:D01279), mRNA
eerusens
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Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Miaon RX
Washington University School of Medicine
Washington University School of Medicine
4444 Sozest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
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Verfebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
1. 289
                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/clone="161660"
15 a 42 c 42 g 40
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//ocem'Organ; bancrass, Vector: pBluescript SK-; Site_1:
//coli; Site_2: MoI"
//db_xref="Amc (inhost):191281"
//db_xref="taxon:980s"
//clone_lbb=roaces tumor I"
//clone_lbb=roaces tumor I"
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US-08-836-455-1.rst

Norak, D.L., Kunsch.C., Rungjun, J., Li.H., Mciannz, P.S., Olsen, H., Raymond, L., Welt, Y.F., Ming, J., Xi, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fancon, M.R., Rosen, C.A., Haseltine, M.A., Fields, C., Fraesz, C.H., and Ventez, J.C., Rosen, C.A., and Ventez, D.H. and expression patterns based upon 83 million nucleotides of CDNA sequence secure 377 (6547 Suppl.), 3-174 (1995)

Bioinformatics
The Institute for Genter Drive, Rockville, MD 20850 USA
712 Hedical Center Drive, Rockville, MD 20850 USA
721: 301859956
Fax: 301859451 up. org.
Fax: 30185951 up. org.
Fax:

ACCESSION NID NEYWORDS SOURCE

H25744 166 bp mRNH,
yl50all.rl Homo-septems CDNA clone 161660 5' smilar to
yl50all.rl Homo-septems CDNA clone 161660 5' smilar to
BP.KVLJ-KVANN PO1602 IG KAPPA CHAIN PRECURSOR V-I REGION ;.
H25744 LWDANN PO1602 IG KAPPA CHAIN PRECURSOR V-I REGION ;.
989487
EST.
EST.
buman clone=161660 library=Goares breast JNbHBst vector=pT7TJD

RESULT 34
LOCUS
DEFINITION

Ouery Match 5.5%, Score 24; DB 24; Length 413; Best Local Similarity 100.01; Pred No. 3.19-17; Ength 413; Marches 24; Conservative 0; Mismatches 0; Indels 0; Gaps

/dev\_stage="adult" <1..>413
100 a 110 c 105 g

3 8¢

1. 413
/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="List Subsite Vector: pBluescript SK-; Site\_1:
EcoRi; Site\_2: Xhoi
/db\_xref="Atoc (inhost):191658"
/db\_xref="Lib="Testis timor"
/sex="male"
/sex="male"

FEATURES source

Seq prime

ion/Qualifiers

il: arbelavetigr.org clone availability, additional sequence and expression commation related to this EST, please check the TIGN Human Gene ex (http://www.tigr.org/cdb/hgi/hgi.html) primer: Hi3 Reverse.

Mon Apr 19 13:23:50 1999

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NID
KEYWORDS
SOURCE
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LOCUS A337254 334 bp mRNA ESTI 20-APR-1997
DEFINITION EST30547 Color 1 Homo eapiens CDNA 5' end similar to similar armonophobulin kappe light chain, V region (GB:LO1279), mRNA ACCESSION A327254 ...
MID 91974499 4:
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Best Local Similarity 100.0%; Pred. No. 4.46e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK

WashD-here No SUP project

WashIngton Dark Parkway, Dox 8501, St. Louis, MO 63108

Tel: 314 286 1800

PAX: 314 286 1800

PAX: 314 286 1810

Each Consortion, LIAU

This clone is available royalty-free through LIAU; contact the This Connection (LIAU Consortion) (L
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Romo.

1 (bases 1 to 334)

Adams.M.D., Kerlavge,A.R., Fleischmann,R.D., Fuldner,R.A., J. Ball,C.J., Lee, N.H., Kirhees,E.F., Weinstock,K.G., Gocayne,J.D., Bhlt,C.J., Lee,N.H., Kirhees,E.F., Weinstock,R.G., Man-Rai,C., Man-Rai,C., Sutton,G., Blake,J.A., Brandon,R.C., Man-Rai,C., Fine,I.D., Clayron,R.A., Cliner,R.R., Cotton, M.D., Earle Highes, J.F., Geoghagen, N.S., Fittsgreald,L.M., Fitchingh,M.M., Fritchman,J.L., Geoghagen,N.S., C., Liu,L.-I., Marmarces,S.H.Niel,P.S.JT., Glodek,A., Gehma,C.L., Hanna,M.C., Hanna, H.C., 
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Homo sapiens
Eukaryotas; mitochondrial eukaryotes; Metasoa; Chordata;
Verrebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae;
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(base; C. t. 2018).

Hillera; C. t. 2018, Dubbque; T. Elliston, K., Hawkins; M., Hadman, M., Hulman, M., Walban, T., Le, M., Lennon, G., Marra; M., Parsons, J., Hithin, L., Nochan, T., Le, M., Lennon, G., Marra; M., Parsons, J., Hithin, L., Rohling, T., Soares; M., Tan, F., and Wilson; R., Waterston; R., Williamson, A., Wohldmann, P. and Wilson; B., Waterston; R., Williamson, A., Wohldmann, P. and
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Seq primer: Mil Reverse
Location/Qualifiers
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Y/61907 tl Room eapless CHUN clone 169780 5; similar to gb:X06764
IG KAPPA CHAIN PRECURSOR V-III REGION (HUNAN);:
H27642 1897995
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/clone="162780"
a 113 c 80 g 70
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ACCESSION AA32143V
NID 91973783
KETWORDS EST.
SOURCE Homo sapiens
ORGANISH Homo sapiens
CHARTOGRE IN
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AUTHORS
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LOCUS
DEFINITION
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Best Local Similarity 91.79; Pred. No. 4.52e-13;
Matches 22; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abuthave A. C. 1929, A. Prischmann R.D. Puldner R.A. 1920, Marchave R.C. 1920, M. 19
SACISED (NO. 1972)

Other_ESTS. PRICES 177

Contact: Kariavge, AR

Bioinformatica for Genomic Research

772 Hedical Center Drive, Rockville, MD 20850 USA

721: 301859058

Fax: 301859413

Email: arkerlavetigr.org
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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lams, M.D., Kerlavi
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2 Bone marrow Homo sepiens cDNA 5' end similar to
2 bbulin kappa light chain, V region, mRNA sequence.
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Apr 19 13:23:50 1999 US-08-836-455-1.rat

Small, N. V., Sprisge, T.A., Utterbeck, T.R., Weidman, J.F., Li, Y., Bednark, D.P., Cao, L., Cepeda, M.A., Collins, E.J., Dinke, D., Peng, D. F., Perrie, A., Pischer, C., Hastings, G.A., He, W.M., Bu, J.S., Greene, J.M., Gruber, J., Hadon, P., K.A.A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Oleen, H., Raymond, L., Wei, Y.F., Walp, J., Xu, C., Yu, G.L., Ruben, S. M., Dillion, P. J., Fannon, M.R., Rosen, C.A., Haseltine, M.A., Fields, C., Fraber, C.M. and Venter, Jo. Thuman gene diversity and expression patterns based upon 83 mallion nucleotides of CDMA sequence securing 177 (6547 Suppl), 3-174 (1995)

Contact: Kerlavage, AR
Bioinformatica
The Institute for Genomi
9712 Medical Center Driv
Tel: 30189905
Fax: 301899943
Email: arkerlaytigr.org for Genomic Research Center Drive, Rockville, MD 20850 USJ Es

Email: arkerlavetigr.org
for clone availability, additional sequence and expression
information related to this EST, please check the TICR Ruman Gene
index (http://www.tigr.org/cdb/Ngi/Ngi.html)
for primer: 1.13 hayerses.

Gorganizam\*Homo esplens\*
//sotam\*Gogin; colon; Vector: pBluescript SR-;
/sotam\*Gogin; colon; Vector: pBluescript SR-;
/db\_ref\*\*Inc (inhost):127923\*
/db\_ref\*\*Inc (inhost):127923\*
/db\_ref\*\*Inc (inhost):17923\*

83 g 4 1 others

Query Match 4.8%; Score Best Local Similarity 100.0%; Pred. Matches 21; Conservative 0; N re 21; DB 24; Len d. No. 4.46e-11; Mismatches 0; Length 334; Indels .

RESULT 38

LOCUS AA335086 345 bp BRNA EST 21-APR-1997

DEFINITION EST39457 Esophagus tumor Homo sapiens CDNA 5' end similar to 
Lemnnoglobulin kappa light chain, V region, ENNA sequence. 
ACCESSION AA335086

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NID REYWORDS SOURCE ORGANISM

Page 70

Gaps

KEYWORDS

KEYWORDS

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MANUAL

MANUAL DEFINITION F1-249D 22 wesk old human fetal liver cDNA library Query Match 4.8%, Score 21, DB 15, Length 395; Best Local Similarity 95.5%, Pred. No. 4.66e 11; Matches 21; Conservative 0; Minmatches 1; Indels 0; Contact: Ree-Sup shin .
Devalopmental Centica .
Penhang Institute of Science & Technology .
Sanil, Nyosdomp Pohang, 790-784 Republic of Korea .
Tel: 562-279-2319
Eax: 562-279-2319 human. Romo ampiens Exkaryotae; mitochondrial eukaryotas; Matazoa; Chordata; Veriebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; oinformatics is Institute for Genomic Research 12 Medical Center Drive, Rockville, MD 20850 USA 1: 3018699056 /organism="Homo sapiens" <1. .>395 87.a 110 c 95 g 96 shinhsevision.postech.ac.kr ner: T3 primer. Location/Qualifiers 1. 202 arkerlayetig; org one availability, additional sequence and expression ation related to this EST, please check the TIGE Human Gene http://www.tigr.org/tdb/hgi/hgi.html) iner: Hil Reverse. Location/Qualifiers /Organism\*\*Homo sapiens\*
/Note\*\*Organ: esophagus: Vector: pBluescript SK-, Site\_1:
/Not\*\* Site\_1: /Not\*\*
//db\_xref\*\*Arc (lahost):136812\*
/db\_xref\*\*Texon:9506
/dor\_site\_18\*\*Exophagus tumor\*
/dev\_stage=\*adult\*\* /organism="Homo sapiens" /note="Vector: pBluescripII SK(-); Site\_1: EcoRI; Site\_2: KhOI; The cDNA library made by oligo-dT primed and 95 g 96 t US-08-836-455-1.rat 7 others expression the TIGR Database 25-APR-1995 Y Komo sapiens Page 71 Page 69 ğ RESSILY AL 294819 259 bp mRNA EST 18-APR-1997
DEFINITION ESTIONS parcreas tumbr I Homo aspiens cDDA 5' end similar to
similar to immunoglobulin kappa light chain, V region (GB:RD2096),
ACCESSION AL294819 necession (GB:RD2096),
RID 91947251
EXTYROLD 51. Mon Apr 19 13:23:50 1999 REFERENCE AUTHORS REFERENCE AUTHORS TITLE Apr 19 13:23:50 1999 RIPHORDS #27 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 RESULT 39

LOCUS 793112 395 bp mRNA EST 06-SEP-1995

LOCUS 1919134 Homo espiens cDNA 5' end similar to immunoglobulin kappa

ACCESSION 799112 (BM V region (GB NO2096) (HT.3818).

ROCESSION 799112 (BM V region (GB NO2096) (HT.3818). Query Match 4.6%; Score 20; DB 21; Length 202; Best Local Similarity 100 0%; Pred. No. 13ee 0; Indels Matches 20; Conservative 0; Missanthes 0; Indels Ouery March Office 4.8%; Score 21; UB 25; Length 345; Best Local Similarity 100 0%; Pred No. 4.466-11; Matches 21; Conservative 0; Himatches 0; Indels 0; Ed Nome

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Bull, C.J., Lee, R., Kirkness, E.F., Weinstock, K.G., Googne, J.D.,
Bull, C.J., Lee, R., Kirkness, E.F., Weinstock, K.G., Googne, J.D.,
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Ittlingh, M.M., G., Hedblom, E., Hihle IT, P.S.,
Weilder, J.M., Moreno-Palanques, R.F., McDonald, L.J., Marmaros, S.M.,
Perick, J.M., Moreno-Palanques, R.F., McDonald, L.J., Mayen, D.T.,
Sedegrino, S.M., Phillips, C.A., Payder, S.E., Soott, J.,
Weilder, J.M., Shitley, R., Small, R.V., Spriggs, T.A., Utterback, T.R.,
Weilder, J.M., Shitley, R., Small, R.V., Spriggs, T.A., Utterback, T.R.,
Weilder, J.M., Shitley, R., Small, R.V., Spriggs, T.A., Utterback, T.R.,
Coleman, T.S., Collin, B., Man, H., Mayer, S.E., Goette, J.H.,
Fischer, C., Hattings, G.A., Weilder, J., Wille, J., Weilder, J., Wille, J., Wille human. Romo sapiens Zukaryotas: mitochondrial sukaryotes: Metasoa: Chordata; Vertebrata: Mammalia; Butheria: Primates: Catarrhini: Hominidas; Eukaryotae: Metasoa; Eumetasoa; Bilateria; Coelomata; Deuterostenia; Chordata; Vertebrata; Garchostomata; Osteichthyes; Sarcopterysi; Chomata; "Tetrapod; Amniota; Mammalia; Theria; tutheria; Archonta; Primates; Caterihin; Romanidae; Romo.

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Adams, M.D., Reilaväge, A.R., Fleischmann v itial assessment of human gene diversity and expression patterns sed upon 83 million nucleotides of cDNA sequence B1 a 100 c 79 g 85 t US-08-836-455-1.ret US-08-836-455-1.rst fetal liver cDNA library Indels 0; Gaps

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0450 2857: TREC18977
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Page 73

Mon Apr 19 13:23:50 1999

Page 74

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A365972 208 bp mRNA EST 21-App.1997

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Best Local Similarity 100.0%; Pred. No. 2 B8-07;
Matches 19; Conservative 0: Mismatches 0; Indels 0;
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Best Local Similarity 100 0%; Pred. No. 348e-09;
Matches 20; Conservative 0; Mismatches 0; Indels
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J. Lee, M. H., Kirkness, E. F., Weinstock, R. G., Goodyne, J. D., White, O. Stron, G., Blake, J. A., Brandon, R. C., Man-Sai, J. F., Fitegerald, T. S., Cotton, H. D., Exrie-Hughes, J., Fine, L. D., Fitegerald, L. M., Fittenband, L. Goodynes, N. S., Glodek, A., Gohm, G. L., Hands, M. C., Redblom, E., Rinkle, P. S. J., Kelley, J. M., Kelley, J. C., Liu, L. I., Karmaros, S. M., Merrick, J. H., Worzeno-Palanques, R. F., McChonald, J. A., Mynyen, D. T., Pelligirlo, S. M., Horzeno-Palanques, R. F., McChonald, J. A., Mynyen, D. T., Pelligirlo, S. M., Shilley, R. A., Robert, J. C., Suder, S. E., Scott, J. L., Sudek, D. M., Filley, R. J., Shilley, R. J., Pallillian, C. A., Fiders, S. E., Scott, J. L. Sudek, D. M., Killey, R. J., Pallillian, P. J., G. L., Raylon, T. A., Loghlan, E. J., Dalkeri, P. S., Gosen, C. A., Haest, S. M., Kosek, D. L., Knash, C., Manglun, J. L. H., Melsaner, P. S., Osen, R., Raymond, L., Wel, T. F., Ming, J., Xu, C., Tu, C. L., Ruben, S. M., Kosek, D. L., Knash, C., Manglun, J. L. H., Melsaner, P. S., Osen, R., Raymond, L., Wel, T. F., Ming, J., Xu, C., Tu, C. L., Ruben, S. M., Kosek, D. L., Knash, C., hand of venter, J. C. Fraser, C. M. and Venter, J. G. human gene diversity and expression patterns bated upon 83 million nucleotides of CNM sequence

All Rature 377 (547 Suppl.) 3-174 (1995)
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Homo sapiens
Eukaryotas; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Karmalia; Eutheria; Primates; Catarrhini; Hominidae;
Contact: Rerlayage, AR
Bioinformatics
The Institute for Genomic Research
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RESULT 42

A294843 279 bp mRNA EST 18-APR-1997

DETINITION ESTI00050 Pancress tumor I Homo septens cDNA 5' end similar to similar to immunoglobulin kappa light chain, V region (GB:RO2096), ACCESSION AA294843

NID ND 9347250

RETWORDS EST.

human. Homo depiens Elkaryotae: mitochondrial eukaryotes; Retaroa; Chordata; Perrebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;

1 (bases 1 to 279)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Puldner,R.A.

Query Match 4.6%; Score 20: DB 24: Length 269; Best Local Similarity 100 0%; Pred. No. 38et-09; Matches 20; Conservative 0: Mismatches 0; Indels 0;

72 g 62 t

/organiame\*Romo sapiens\*
/mote="organ: pancreas: Vector: pBluescript SK-: Site\_1:
DooRI: Site\_2: KhoI'
/db\_xre="wfxc (inhost):190400\*
/db\_xre="wfxc (inhost):190400\*
/db\_xre="wfxc (inhost):190400\*
/db\_xre="wfxc (inhost):190400\*
/dev\_process (umor I'
/dev\_process adult'

ation/Qualifiers 269

REYWORDS SOURCE ORGANISM

ACCESSION NID RESULT 43
LOCUS
DEFINITION

729212 174 bp m884, 257 06-SEP-1995 EST-7046 Homo sapiese COMA 5' end similar to immunoglobulin kappa light chain, V region (GB:Y00640) (HT:3112). 729212 1857.

Apr 19 13:23:50 1995

71 TGACCCAGTCTCCATCCTCC

KEYWORDS SOURCE ORGANISM

ISS Muman primer=Mil Reverse library=Human Ovary.

Homos espiens

Eukaryonas Mecasoa, Eumetaroa, Bilateria, Coelomata, Ostelohiyes, Eukaryonas, Mecasoa, Eumetaroa, Salateria, Contontonia, Chordata, Ferrebrett, Gnethostomata, Ostelohiyes, Eukaryonas, Pythonio, and Reinalia, Chordata, Ferrebrett, Gnethostomata, Ostelohiyes, Butharyan, Butharyan, Bandon, R. D., Berther, B. D., Berther, B. D., Bathopher, M. D., Bartharyan, B. D., Filder, B. D., Bathopher, B. D., Bathopher, B. D., Bathopher, B. D., Batharyan, B. Bandon, R. D., Pilder, B. D., Calven, M. D., Batharyan, B. Bandon, R. C., Chiu, M. W., Clyton, R. A., Cline, R. T., Cotton, M. D., Batharyan, J. Googland, D., White O., Batharyan, B. Bandon, R. C., Chiu, M. W., Clyton, R. A., Cline, R. T., Cotton, M. D., Batharyan, J. Googland, J. B., M. G., Gharyan, J. Googland, J. S. M., Kilnek, K. M., Kalley, J. C., Liu, L. T., Marmaros, S. M., Kerley, J. M., Klinek, K. M., Kalley, J. C., Liu, L. T., Marmaros, S. M., Kerley, J. M., Klinek, K. M., Klinek, K. M., Kalley, J. C., Liu, L. T., Marmaros, S. M., Kerley, J. M., Klinek, K. M., Klinek, K. M., Klinek, C., Chu, J. K., Kerley, J. M., Colline, E. M., Klinek, K. M., Klinek, K. M., Klinek, C. M., Sprigge, T. A., Uterback, T. R., Colline, E. M. M., Colline, E. M., Colli

FEATURES source

/organism="Homo sapiens" <1. >174

Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gathersbury, ND 20978
Tel: 3018599055
Pax: 301859905
Pax: 301859905
Tel: 40binCottoh: tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TICR Database
(cdbinfoetdb.tigr.org)
Location/Qualifiers

REFERENCE AUTHORS

Gaps

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Page 78
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В
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BASE COUNT
ORIGIN
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LOCUS
DEFINITION
                                                                    Obery Match 44%; Score 19; DB 24; Length 253;
Best Local Similarity 100 (N); Pred Mo. 283-07;
Matches 19; Conservative 0; Minmatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apr 19 13:23:50 1999
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1 (bases 1 to 253)

Admin, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Admin, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Balle, D., Kerlavage, A.R., Fleischmann, R.D., Kan, Kal, Googayne, J.D.,

Balle, D., Kerlavage, M.R., Bridden, R.C., Kan, Wal, C.,

Kultron, R. A. (Colies, T.R. Are, J.A.), Brandon, R.C., Kan, Wal, C.,

Friegread, A.M., Gelma, C.L., Hanna, M.C., Friedham, E., Hirdysten, M.S.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Hannaros, S.M., Merrick, J.M.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Hannaros, S.M., Merrick, J.M.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Hannaros, S.M., Merrick, J.M.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Hannaros, S.M., Merrick, J.M.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Hannaros, S.M., Merrick, J.M.,

Benali, K., Sprigge, T.A., Otterback, T.R., Weidman, J.F., Lif, Y.,

Benali, M., Sprigge, T.A., Otterback, T.R., Weidman, J.F., Lif, Y.,

Benali, M., Sprigge, T.A., Otterback, T.R., Weidman, J.F., Lif, Y.,

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Benali, M., Sprigge, T.A., Otterback, T.R., Weidman, J.F., Lif, Y.,

Benali, M., Sprigge, T.A., Otterback, T.R., Weidman, T.A., Collins, E.J.,

Benali, M., Sprigge, T.A., Otterback, T.R., Weidman, T.A., Collins, E.J.,

Benali, M., Sprigge, T.A., Otterback, T.R., Weidman, T.A., Collins, E.J.,

Benali, M., Sprigge, T.A., Otterback, T.R., Weidman, T.A., Collins, E.J.,

Benali, M., Sprigge, T.A., Otterback, T.R., Weidman, T.A., Collins, E.J.,

Benali, M., Sprigge, T.A., Otterback, T.R., Weidman, T.A., Collins, E.J.,

Benali, M., Sprigge, T.A., Otterback, T.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kerlavage, AR
Bloinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018659056
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yj39503.r1 Homo saptems croba clone 155332 5' similar to gb:L09085 R69482 R69482
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Deutezostonia, Ghordata; Vertebrita; Ganthostomata; Osteichthyes;
Sarcoprerygii: Choanata; Tetrapoda; Amniota; Mammalis; Theria;
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Tel: 301689943
Email: alterlawitigs.org
Additional sequence and expression
information related to this EST, please check the TIGR Human
Index Intel: //www.tigs.org/tdb/hgi/hgi.html)
Seq primer: MJ Reverse.
1. 2081 Reverse.
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//organizam; thymus. Vector: pBluescript SK-; Site_1:
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A295941 255 bp mRN, EST 18-APR-1997

DEFINITION ESTIDIES Thymus III Homo sapiens CDN, 5 end similar to similar to similar to similar to immunoglobulin kappa light chain, V region (GB: F00640), mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E 1 (bass 1 to 328)

3 Adams.H.D., Kerlavage.A.R., Fleischmann.R.D., Fuldner,R.A.,

5 Adams.H.D., Kerlavage.A.R., Fleischmann.R.D., Fuldner,R.A.,

5 Malms.H.D., Kerlavage.A.R., Caten.R.C., Wan Wal.C.,

6 White.O., Sutton.G., Blake.J.A., Brandon.R.C., Man Wal.C.,

6 Clayton.R.A., Cline.T.R., Cotton.M.D., Exit-luybes.J.,

7 Clayton.R.A., Cline.T.R., Cotton.M.D., Exit-luybes.J.,

8 Clayton.R.A., Flethugh.R.M., Fritchmann.J.L., Geoghagen.N.S.,

9 Clock.A., Gashm.C.L., Hanna,M.C., Hedblon.J., Hindle, P.S.J.,

8 Clock.A., Cashm.C.L., Hanna,M.C., Hedblon.J., Hindle, P.S.J.,

8 Clock.A., Robert.S.E., Scott.J.L., Saudek.D.R., Shriey.R.M.,

8 Mall.R.W., Spriggs.J.A., Utterback.T.R., Wetdman.J.E., Lify.R.,

9 Bendarik.D.P., Cao,L., Cepeda.M.A., Colemn.T.A., Collins.E.J.,

10 Jake.D., Feng.D.F., Ferris.A., Guber.J., Haddon.J.R., E.J.,

11 Jake.D., Feng.D.F., Ferris.A., Guber.J., Haddon.J.R., Kin.A.,

12 Raymond.L., Well.Y.F., Sing.J., Xu.C., Yu.G.L., Ruben.S.M.,

13 Raymond.L., Well.Y.F., Sing.J., Xu.C., Yu.G.L., Ruben.S.M.,

14 Partial Namearment of Numan cane diversity and expression matterns

15 Trial Nameamment of Numan cane diversity and expression matterns
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Washinger, Spr. servicet
Wa
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Contact: Kerlawge, AR
Bloinformatice
Floring Contact Research
Floring Contact Research
Floring Contact Research
Floring Contact Drive, Rockville, ND 20850 USA
Fal: 3018699421
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EST20808 Spleen I Homo sapiens cDNA 5' end a
immunoglobulin kappa light chain, V region (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thitial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDMA sequence Mature 377 (6547 Suppl), 3-174 (1995)
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Romo aspens
Eukaryotae: mitochondrial eukaryotes: Metazoa: Chordata;
Vertebrata; Mammalia; Eutheria; Primates: Catarrhini; Hominidae;
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Ebkaryotae: mitochondrial eukaryotes: Metazoa: Chordata;
Vertebrata: Mammalia: Eutheria: Primates: Catarphini: Hominidae;
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The WashU-Merck EST Project Unpublished (1995)
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1 (bases 1 to 210)

Hillier, L., Clark, M., Dubuque, T., Elliston, K., Havkins, H.,

Holman, M., Maltman, M., Kucaba, T., Le, M., Lenno, G., Marra, M.,

Parsons, J., Hitthin, L., Rohlfing, T., Geares, M., Tun, F.,

Trevaskin, E., Waterston, R., Williamson, A., Wohldmann, P. and

Wilson, R.
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/clone="155332"
53 a 56 c 46 g 50
kerlav@tigr.org
availability, additional sequence and expression
on related to this EST, please check the TIGR Human Gene
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Koeak, D. L., Kunesh, C., Hungdun, J., Li, H., Meissner, P. S., Olsen, H., Raymond, L., Watt, P. S., Watt, J., Xu, C., Yu, G. L., Ruben, S. M., Dillion, P. J., Pannon, M. R., Rosen, C. A., Haseltine, W. A., Fields, C., Fraer, C. M. and Venter, J. C., Think, A., Rosen, C. A., and expression patterns based upon 33 million nuclectides of CDNA sequence Macure 377 (6547 Suppl.), 3-174 (1995)

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Page 82
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ACCESSION AA300732

NID 91933300

RETWORDS EST.

SOURCE human.

ORGANISH Homo sapiens
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Best Local Similarity 100.0%; Pred. No. 2.188-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0;
(Pharmacia) with a modified polylinker host-DHIOD (ampicillin resistant) primer=MIRD1 Raitel=MOC I Raitel=MOC RI Adult human.

IT STATEMENT DEFINED WITH A MOC I Raitel=MOC RI Adult human.

IT STATEMENT DEFINED WITH A MOC I RAITENET TO JUDICAL THE MOC AND ADDRESS OF THE MOC 
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RE dalman, R.D., Escalusgo, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bultza, M.D., Lean H. H. Efferens E.F. when took K. Goldon, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Mad.C.,
Clayton, R.A., Cline, T.R., Cotton, H.D., Earle-Rughes, J., Fine, L.D.,
Fitzgerald, L.H., Fithwhyb, M.H., Fritchman, J.L., Goodney, S.S.,
Goldek, A., Gohem, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.-J.,
Kelley, J.H., Kelley, J.C., Liu, L.I., Marmares, S.H., Merrick, J.H.,
Morzeno-Palaques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.H.,
Horzeno-Palaques, R.F., McDonald, L.A., Nguyen, D.T., Felligrino, S.H.,
Shillips, C.A., Ryder, E.E., Scott, J.L., Saudek, D.H., Shirley, R.,
Bullik, V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., LLT,
Bedhall, D.D., Cool, L., Cepeda, M.A., McColeman, T.A., Colling, E.J.,
Dedhall, D.D., Cool, L., Cepeda, M.A., McColeman, T.A., Colling, E.J.,
He, M.M., Bu, J.S., German, M.N., Scher, C., Mastell, M.R.A.K.,
He, M.M., Bu, J.S., Caren, J.H., College, J., McMoo, P., Man, A.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Nilson RK.

NashD-Merck EST Project

WashIngton Dniversity School of Medicine

444 Forset Park Parky, Box 8501, St. Louis, NO 63108

Tel. 314 286 1800

Par: 314 286 1810

Enail: estewason wustl.edu

High quality scuence strops: 23

Source: 1206E consortius ryally free through LiMi; contact the

INGE Consortium (info@image.lini.gov) for further information.

Losation/Qualifiers

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g1953300
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Seq primer: M13 Reverse.
                                                                                                                        19: Conservative O: Kismatches O: Todis O: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The WashU-Merck EST Project 
Unpublished (1995)
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Vertebrata; Mammalia; Eutheria; Primatea; Catarrhini; Hominidae;
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                          The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 Tel: 1018699058 Fax: 301869923 Fax: 301869924 Fax: 30186974
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Boall: arkerivettger.org
Bor clone availability, additional sequence and expression
information relaxed to this EST, please check the TiGR Human Gene
Index (http://www.iigr.org/thb/hgi/hgi.html)
Seq primer: M1 Reverse.
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The Institute for Genomic Research 97/2 Heddical Center Drive, Rockville, ND 20850 Tel: 301859943 Fax: 301859943 Eastl: atheriastigs.org Ror clone availability, additional sequence and Ror clone availability, additional

Email: arkerlaretty; org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/db/hgi/hgi.html) Seq primer: H3.1 Reverse. Goottion/Qualifiers

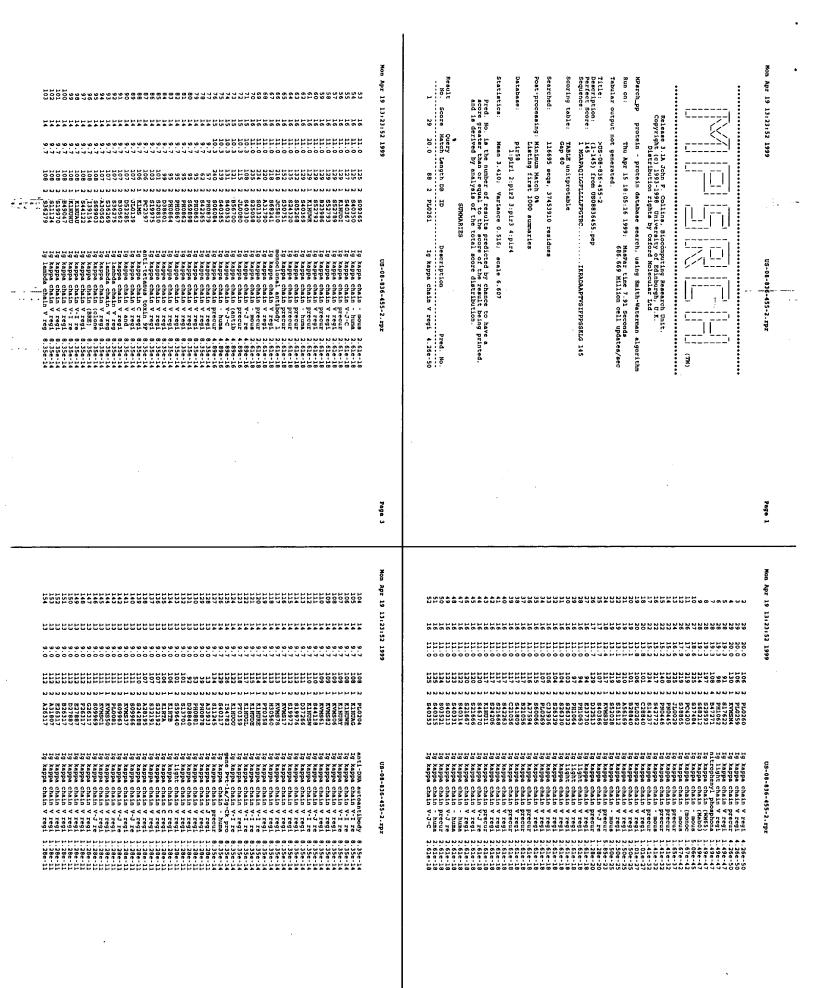
oryanism="Homo sapiens" oryanism="Homo sapiens" note="Organ: testis: Vector: pBluescript SK-; Site\_1: coRI; Site\_2: XhoI"

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PIR2: PL0261
PIR4: B47271
PIR2: PH1062
PIR1: PH1062
PIR1: KVMS3B
PIR2: B28840
PIR2: C28840
PIR2: C28840
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NBRF, Release 58.0, Released on 30Sep1998, Formatted on 15Dec1998

Word-size: 5 Words: 49743 Diagonals: 7,036 Total diagonals: 54,270,613 (Integral-width: 1 Alphabet: 20 List-size: 50 CPU minutes: 4.54
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2:S09365
2:S2986
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\*fournal Science (1957) ISS 465-467 Rood, L.

\*fittle Mechanism of unibody synthesis: size differences between the chains of unibody synthesis: size differences between the construction of unibody synthesis: size differences between the c REFERENCE A53815

\*\*Journal Proc. Nail Acad. Sci. U.S.A. (1977) 74:715-720

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An Lemmoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, garma, or mu) chains usually stabilised by interchain disulfide bonds. In some cases, such as 15A and 15M, the subunits associate into larger oligomers. 24-bpr-1984 sequence\_revision 24-bpr-1984 stext\_change 15-hug-1995 appr-1984 stext\_change 15-hug-1995 appr-1984 stext\_change 15-hug-1995 appr-1981; A93815; A94239; A01922; A01923 appr-1111 apprentice for the following steams of the following steps apprentice for the following steps apprentice fo Shamchik, M.; Mascelli, M.; Shan, H.; Radio, M.Z.; Pietsky, D.; Marshak-Rothstein, A.; Weigert, M.
2 Exp. Med. (1990) 177:265-98:59ert, M.
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Shlomchik, M.: Maicelli, M.; Shan, H.; Radio, M.Z.; Pisetaky, D.; Marshak-Rothstein, A.; Weigert, M.
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Making antibody fragments using phage display libraries.
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#disulfide\_bonds #status predicted #length 108 #checksum 9036

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888211 Takagi, M.; Robda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, H.; Tannaka, T. EBS Lett. (1995) 373:273-276

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etitle Thermostable peroxidase activity with a recombinant antibody L. chain-porphyrin Fe(III) complex. 868112

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PH0971, D.K.; Jou, N.T.; Hill, R.J.; Marion, T.N.
Tillan, D.K.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. (1992) 176:781-779
Both Jeff and 19G anti-DNA antibodies are the products of clonally selective B cell stimulation in (NEB x NEW)FI
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Lealey, S.A.; Patten, P.A.; Schultz, P.G. Proc. Natl. Acad. Sci. U. S.A. (1993) 90:180-1165 A genetic approach to the generation of antibodies with schanced catalytic activities. Tops. MUID:9316566

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ROAD M: Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.;

#ournal Gene (1996) 173:577-28

#fitte light chains do monotional antibody (MAMA4) Specific for human plasma apolipoprotein A-I.

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\*\*State Desky mutations cause the somatic diversification of 19M and corrected with the santiphosphorylaboline antibodies.

\*\*Gross-references MUID:881/1315

\*\*Accression JJ0029

\*\*\*Molecule\_type mRNA

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Combination of a defined specificity and desired incrype by
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Antibody.

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#domain signal sequence #status predicted #label SIGN #product Ig light chain kappa-1 V region #status predicted #label NAT #length 128 #checksum 5891

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Gene (1992) 122:321-328
A general method for chimerisation of monoclonal antibodies
by inverse polymerase chain reaction which conserves
authernic N-terminal sequences.
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uza, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle,

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\*\*Ittle Construction and characterisation of a recombinant murine monoclonal antibody directed spainst human fibrin fargment-Dimer.

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\*journal EMBO J. (1995) 4:3681-3688
The iddoxypic network and the internal image: possible resulation of a serm-like network by paucigene encoded Ab2 resulation of a serm-like network by paucigene encoded Ab2 resulation (SAT System. Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Pougereau,

ecrosar-references MVID:86136012

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0111er, P.: Rocca-Serra, J.: Somme, G.; There, J.: Pougereau,

Query Match 13.1%; Score 19; DB 2; Length 101; Beat Local Similarity 90.5%; Pred. No. 2.50e-25; Indels 0; Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps

ORGANISM DATE ACCESSIONS REFERENCE Bauthors NS0189 \*type fragment
Ig kappa chain V region (clone 23.2) - mouse (fragment)
Formal\_name Nus musculus \*common\_name house mouse
19-Oct-1995 \*sequence\_revision 19-Oct-1995 \*text\_change
16-Aug-1996

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B.; Rocenbaum, R.; Godillot, A.P.; Kaushansty, K.; Brown,
C.B.; Voet, D.; McCallue, D.E.; Meiner, D.B.; Williams,
C.B.; Voet, D.; McCallue, D.E.; Meiner, D.B.; Williams, W. V.
J. Biol. Chem. (1995) 270:6628-6638
Recombinant antibodies in bloactive peptide design.
A56169

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Ouery Match 13.1%, Score 19: DB 2: Length 210; Best Local Similarity 100 0%; Pred No. 2.50c-25; October Matches 19: Conservative . 0: Mismatches 0: Indels 0: 108 LEIKRADAAPTYSIFPPSS 126 Gaps

Page 35

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RESULT 20
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B28840 etype fragment
Ig kappa chain V region (BP27) - mouse (fragment)
fformal\_name Nus musculus #common\_name house mouse
29-Aug-1987 sequence\_revision 29-Aug-1987 #text\_change
16-Aug-1995
828840; 135145

Ouery Match 13.8%; Score 20; DB 2; Length 106; Best Local Similarity 100.0%; Pred. No. 1.01e-27; Matches 20; Conservative 0; Mismatches 0; Indels

0 Gaps

ACCESSIONS

124 LEIKRADAAPTVSIPPPSS 142

ORGANISM DATE

ACCESSIONS REFERENCE Sauthors \*\*Whors\* Vasen, M.; Prosch, M.; Weisgerber, C.; Eckart, K.; Kratzin, fournal Modermann, D.; Hissehmann M.; Prosch, M.; Weisgerber, C.; Eckart, K.; Kratzin, fournal Modermann, D.; Hissehmann M.; Modermann, M.; Moderma

KEYWORDS SUMMARY Query Match 13.1%; Score 19; DB 2; Length 219; Best Local Similarity 100.0%; Pred. No. 2.50e-25; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps

RESULT 23
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19 kappa chain - mouse

19 kappa chain - mouse

10 rady 1995 sequence\_revision 21-Jul-1995 etext\_change
77-May-1995 sequence\_revision 21-Jul-1995 etext\_change

\*description van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schotz, A.; Bakker, J.; Gommers, F.J.; Jongsma, M.A.; Bosch, D.; Stietena, W.J. eumbitted to the EMBI Data Library, August 1999 Coordinate expression of antibody submit genes yields high levels of functional antibodies in roots of transgenic

preliminary

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Page 37 Mon Apr 19 13:23:52 1999

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Gaps ..

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REFERENCE MAX. E.; Seidman, J.G.; Miller, H.; Leder, P.

sjournal call (1880) 17,99-799

etitle Variation in the crossover point of kappa immunoglobulin gene
scross-references MID:81064681

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Best Local Similarity 100.0%;
Matches 17; Conservative
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sjournal Proc. Mail. Acad. Sci. U.S. A. (1989) 86:574-6747

Exity rearrangements of genes encoding muzine immunoglobulin

kuppa-cholina, unlike genes encoding heavy chains, use

stribble gene segments dispersed throughout the locus.

secresion E33730-89367325
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Ig kappe chain v region (9.42) - mouse
formal_name Nus musculus ecommon_name house mouse
09-Mar-1990 esequence_revision 18-Sep-1992 etext_change
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An immunoglobulin heteroretramer subunit consists of two identical light (happa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilised by interchain dissuffice bonds. In some cases, such as 19A and 19M, the subunits associate into larger superfamily immunoglobulin V region; immunoglobulin homology heteroretrames.
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Ig kappa chair precursor V region (VRM1738) - mouse

Ig kappa chair precursor V region (VRM1738) - mouse

19 -un-1901 *sequence_revision 29 -un-1991 *text_change

20 -Mar-1992
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Pred. No. 2.61e-18;
0; Mismatches 0; Indels 0;
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J. Exp. Med. (1992) 176:761-779
Both 19M and 19G anti-DNA antibodies are the products of closely selective B cell stimulation in (NZB x NZW)Pl
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19 119th chain 7 region (clone 202.54) - mouse (fragment)

16 ormal_name Mus muscrilus scommon_name house mouse and

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J. Exp. Med. (1992) 176:751-779
Both 1gM and 1gO anti-DNA antibodies are the products of cloudly selective B cell stimulation in (NEB x NEW)?1
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Ig light chain *region (clone 202.33) - mouse (fragment)
dormal_name Mus musculus *common_name house mouse mouse
30-sep-1993 *sequence_revision 30-sep-1993 *text_change
15-yun-1996
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Ig kappa chain precursor v region (BXM18) - mouse

##Cormal_name Nus musculus #common_name house mouse
21-May-1990 #eequence_revision 31-Dec-1990 #text_change
20-May-1990
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Eur. J. Immunol. (1993) 23:3348-3271
Expressed human immunoglobulin chi genes and their
hypermutation.
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J. Clin. Invest. (1988) 82:852-860
Immunoglobulin kappa light chain variable region gene complex
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CLASSIFICATION KEYWORDS FEATURE 1-22 23-117

##note GENETICS #introns COMPLEX

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RESULT 24 ENTRY TITLE ORGANISM DATE

45-110 SUMMARY

Query Match

RESULT 27
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J. Emp. Hed. (1991) 17:613-624

Antibodies that are specific for a single amino acid
interchange in a protein epitope use structurally distinct
variable regions.
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J. Exp. Hed. (1991) 174:613-624
Antibodies that are specific for a
interchange in a protein epitope
variable regions.
S26330
Wien, M.W., Fliman, D.J., Sture, E.A., Guillot, S.;
Delpeyrour, P.; Crainic, R.; Bolge, J.M.
Mature Struct, Blol. (1995) 2-237-241
Mature Struct, Blol. (1995) 2-237-241
Structure of the complax between the fab fragment of a
neutralizing antibody for type 1 policylrus and its viral
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Ig kappa chain V region (monoclonal antibody C1) - mouse
(fragment)
formal_name Mus musculus *common_name house mouse
15 cpmal_name Mus musculus *scommon_name house mouse
13 -pab-1996 *equence_revision 10 -oct-1997 *text_change
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Length 103;

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Score 16: DB 2: Length 104: Pred. No. 2.61e-18; 0: Mismatches 0: Indels

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RESULT 33
ENTRY
TITLE
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C19995 etype fragment
19 kappa chin v region (NY113) - mouse (fragment)
19 kappa chin v region (NY113) - mouse (fragment)
19 tappa chin v region (NY113) - mouse house mouse
19 Mar-1990 sequence\_revision 09-Mar-1990 stext\_change
08-Sep-1997

ACCESSIONS
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RESULT 34
ENTRY
TITLE
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PLO259 Stype fragment 1910-1919 - mouse (fragment) 19 kmps chain X resion (arti-DNA, 3E277) - mouse (fragment) 16 formal\_name Nus musculus scommon\_name house mouse to 16 formal\_name (article) 19 formal 1910 - mouse (fragment) 16 formal 1910 - mouse (fragment) 16 formal 1910 - mouse (fragment) 16 formal 1910 - mouse (fragment) 1910 - mouse (

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1 DIOMTOSPSSLSASIG 16

REFERENCE

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CLASSIFICATION
KEYWORDS
FEATURE
16-95
23-93
SUMMARY #authors Wish, M.W.; Hogle, J.M.
#subhission submitted to the Brookhaven Protein Data Bank, January 1995
#cross-references DPB:JEPT
#cross-references DPB:Je #domain immunoglobulin homology #label IMM #disulfide\_bonds #status experimental #length 115 #checksum 7524 US-08-836-455-2.zpr

Quary Match 11.0%; Score 16; DB 2; Leafth 115; Best Local Schildarity 100.0%; Pred. No. 2.61-18; not the Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps

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ACCESSIONS REFERENCE sauthors ORGANISM DATE A27594 stype complete
Ig Amppa Chain precursor VI region (Malm-6) - human
ig Amppa Chain precursor VI region (Malm-6) - human
ig-Nov-1988 sequence\_revision 19-Nov-1988 stext\_change
16-Aug-1996

# authors Graninger, N. B.; Goldman, P.L.; Morton, C.C.; O'Brien, S.J \*\*

# spournal J. Exp. Med. (1988) 167-488-501

# title The kappa-deleting element. Germine and rearranged, ecross-references MUID: 888154739

# accession A27594

# # spourner was translated from an aberrantly translated this equance was translated from an aberrantly rearranged kappa gene from lambda producing B cells

### spourner was translated from an aberrantly rearranged kappa gene from lambda producing B cells

GENETICS
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CLASSIFICATION #84
KEYWORDS het \*superfamily immunoglobulin V region: immunoglobulin homology heterotetramer; immunoglobulin #domain signal sequence #status predicted #label SIG #length l16 #molecular-weight 12739 #checksum 9571

Query Match 11.0%: Score 16; DB 2; Length 116;

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#accession stitle The V(kappa) genes of the L (kappa) gene sequences in S41809 regions and the repertoire of V the human germ line.

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Query Match 11.0%; Best Local Similarity 100.0%; Matches 16; Conservative Score 16: DB 2: Length 117: Pred. No. 2.61e-18; 0: Mismatches 0: Indels Length 117; 0 Gaps

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1-127 selabel HUB
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1-127 selabel HUB
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CLASSIFICATION KETWORDS SUMMARY #euperfamily immunoglobulin vegion; immunoglobulin homology
heterotetramer; immunoglobulin vegion; immunoglobulin homology
#length 117 #molecular-vegion 12778 #checkaum 5619

Query Match 11.0; Score 15; DB 2; Length 117; Best Local Similarity 100.0; Preds No. 261e-18; Matches 16; Conservative 0; Minatches 0; Indels 0; Gapa

21 RCDIOMTQSPSSLSAS 36

RESULT 39 ENTRY TITLE ORGANISH DATE

C21056 etype fragment
Ig kappa chán precusar v zegion (HK137) - human (fragment)
#foormal\_name Homo sapiens #common\_name man
03-Nug-1990 #sequence\_revision 03-Nug-1990 #text\_change
20-Mar-1998

ettle Prolution of immunojabulin v genes evidence indicating that recently duplicated human V-kappa sequences have diverged secression C21056 secretaring previous pr

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S S Apr 19 13:23:52 1999

19 RCDIONTOSPSSISAS 34

RESULT 40 ENTRY TITLE ORGANISM DATE

ACCESSIONS REFERENCE sauthors

#journal

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wadob type complete g Kappa Chail V Tejon ((0) - human g Kappa Chail W Common Lase man Somal\_hame Komo sapiens Wommon Lase man Somal\_hame Komo sapiens Wommon Ja-Jan-1995 West\_Change () Sep-199

Scott, M.G., orimmina, D.L., McCourt, D.M., Chung, G.;
schachle, K. F.; Thiebe, R.; Quenzel, E.M.; Zachar, H.G.;
Nahm, M. (1991) 147-4007-4013
Clonal characterization of the human igd antibody repercoire
to Hammphilus influence type bolysaccharide. IV. The
less frequently expressed VL are heterogenous.

Query Match 11.0%; Best Local Similarity 100.0%; Matches 16; Conservative Score 16; DB 2; Length 117; Pred. No. 2.61e-18; 0; Mismatches 0; Indels 0;

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21 RCDIQMTQSPSSLSAS 36

RESULT 41
ENTRY
TITLE
ORGANISM
DATE S21668 étype complète 19 kappa cháin V region (64) - human 19 kappa cháin V region (64) - human 27-Nov-1933 ésequence\_revision 10-Nov-1995 étext\_change 08-5ep-1997

Roeschenthaler, F.; Scheeble, R.F.; Thiebe, R.; Zachau, H.G. Biol. Chem. Hoppe-Seyler (1992) 373:17-88 f. Of orphons and UROs. behintation of the germline repertoire of human immunoglobulin Kappa genes.

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Page 45

Page 46

Gaps

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Best Local Similarity 100.0%; Pred. No. 2.61e-18; Matches 18; Conservative 0; Mismatches 0; Indels 0; 21 RCDIQMTQSPSSISAS 36

RESULT 37 ENTRY TITLE ORGANISM DATE B21056 \*type fragment
Ig kappa chain precursor v region (HK134) - human (fragment)
fformal\_name Homo sapiens \*common\_name man
03-Aug-1890 \*sequence\_revision 03-Aug-1890 \*text\_change
20-Mar-1998

ACCESSIONS REFERENCE \*\*authors \*journal \*title 

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RESULT 38
ENTRY
TITLE
ORGANISM
DATE 

ACCESSIONS REFERENCE \*Authors \*journal Hubber, C.; Schaeble, K.F.; Huber, E.; Klein, R.; Meindl, A.; Thiebe, R.; Lamm, R.; Zachau, H.G. Bur. J. Immunol. (1993) 23.2866-2875

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RESULT 42 ENTRY TITLE ORGANISM DATE

DNA sequences of

Query Match Best Local S Matches 1

11.0%; Score 16: DB 2: Length 117: Similarity 100 0%; Pred. No. 2. 51e-18; Conservative 0; Hismatches 0; Indels 0: Gaps

ACCESSIONS REFERENCE \*authors \*journal

\*\*molecule\_type\_DNA
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\*\*erosa-tecences ENEL-X5911: NID:g33252: PID:g33253

\*\*experimental\_source placenta

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##Status prilminary
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Mcindl, A.; Thiebe, R.; Hitsel, S.; Zachau, H.G.

#journal Bur. J. Immunol. (1991) 21:1821-1827

The human immunoglobulin kappa locus. Characterisation of the

erosa-refered duplicated or regions.

december MIDI:91310953
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predicted #label NATN 
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*domain immunoglobulin homology *label IMMN 
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*length 117 #molecular-weight 12799 *pchecksum 7420 
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**surbors**

Benlley, D.L.: Rabbitts, T.H.

sjournal cell (1983) 32:181-89

Projuction of immunoglobulin V genes: evidence indicating that recently duplicated human V-kappa sequences have diverged across-references MUD:83129397

**acrossion Allos6

**smolecule_type DM,

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KEYPORDS heterofetztamer; immunoglobulin 
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etitle Of comploss and URBo. Delimitation of the germline repertoire of human immunoglobulin kappa genes.

**Ecoss-references MUID-92281681
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Biol. Chem. Hoppe-Seyler (1992) 373:177-186
Of orphone and UHOs. Delinitation of the germline repertoire
of human immunoplobulin kappa genes.
Thoman immunoplobulin kappa genes.
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Ig kappa chain precursor vI region (HK101) - human
fformal_name Hemo sapiens #common_name man
31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change
13-May-1997
10.1881: A11056
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Ig kappa cháin V region (3) - human
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27-Nov-1993 ésequence_revision 10-Nov-1995 étext_change
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Nature (1980) 288:730-733
Kiman immunos)obulin variable region genes .
two V-kappa genes and a pseudogene.
volume Maria (1989) 666
Nolume (1981) 81098) 666
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Pred. No. 2.61e-18;
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Page 52

RESULT 44
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Db 21 RCDIQMTQSPSSLSAS 36

Ouery Match 11.0%; Score 16; DB 1; Length 117; Best Local Similarity 100.0%; Pred. No. 2. Sie-18; Matches 16; Conservative 0; Mismatches 0; Indels 0;

38-112 45-110 SUMMARY

Apr 19 13:23:52 1999

US-08-836-455-2.zpr

ACCESSIONS REFERENCE \*authors \*journal \*title

Bensimon, C.; Chastagner, P.; Zouali, M. EMBO J. (1994) 13:2951-2962 Human lupus anti-DNA autoantibodies undergo essentially primary V(chi), gene rearrangements. ) h

364370 \*trpe fragment (723-9) - human (fragment)
10 kmpa chain v3 region (723-9) - human (fragment)
10 kmpa chain v3 region (723-9) - human (fragment)
17-Jan-1935 sequence\_revision 01-Sep-1935 \*text\_change
08-Sep-1935 sequence\_revision 01-Sep-1935 \*text\_change
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Ouery Match 11.0%; Score 16; DB 2; Length 120; Best Local Similarity 100.0%; Pred. No. 2.61e-18; Matches 16; Conservative 0; Mismatches 0; Indels

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Score 16; DB 2; Length 120;

9 RCDIQMTQSPSSLSAS 24

S21666 stype complete
Ig kappa chain V region (Z2) - human

ACCESSIONS REFERENCE \*Authors \*journal \*title

RESULT 47
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Query Match 11.0%; Score 16; DB 2; Length 124;
Best Local Schilarity 100 00; Pred No. 2.512-18;
Matches 16; Conservative 10; Mismatches 0; Indels 0; Gaps
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                                                                         #domain signal sequence *status predicted *label SIC\
*product ig kapa chain V region *status predicted
*label MATN v segment *label VSE\
#domain J segment *label VSE\
#distillate_bonds *status predicted
#length 124 *checksum $886
                                                                                                                                                                                                                   #superfamily immunoglobulin V region: immunoglobulin homology heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                   Addhalov, V.A.; Stepchenko, A.G.; Deev, S.A.; Polyanovskii, O.L., 
O.L., 
Wol. Bkol. (1987) 21:945-948
Structure of the variable gene coding for chi-chains of 
antibodies produced by hybridoma PTP-02.
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Ig kappa chain - human
Ig kappa chain - human
Formal_name Rome sapiens @common_name man
06-Mar-1994 @sequence_revision 26-May-1995 @text_change
08-5ep-1997
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Eur. J. Immunol. (1993) 23:3348-3371
Expressed human immunoglobulin chi genes and their
hypermutation.
$40331
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Klain, R. Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. (1993) 23:3248-3371
Expressed human immunoglobulin chi genes and their
hypermutation.
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19 kappa chain - human
19 kappa chain - human
16 kappa chain
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Best Local Similarity 100; Pred No. 2 (51-21)
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps
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Best Local Schilarity 100.0%; Pred. Bo. 2.61e-2, DB 2;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps
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540312

Klain, R.; Jaenichen, R.; Jachau, H.G.

Euric, Immunol. (1999) 23:3248-3271

Expressed husan immunojobulin chi genes and their

Dipermutation.
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If kappa chain precursor V region (hybridoma PTF-02) - mouse
(fragment)
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Ig kappa chain vJ region human
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20-Mar-1998
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Mon Apr 19 13:23:52 1999

ACCESSIONS REFERENCE \*authors \*journal \*title

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ORGANISM DATE

ACCESSIONS REFERENCE \*authors

Search completed: Thu Apr 15 18:06:05 1999 Job time : 49 secs.

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GENESEQP: w16620
GENESEQP: w11815
GENESEQP: w01171
GENESEQP: w001033
GENESEQP: w600033
GENESEQP: w350303
GENESEQP: w35130
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Geneseq-AA, Release 34.4, Released on 4Feb1999, Formatted on 5Feb1999
Word-size: 5 Words: 56705 Diagonals: 5,617 Total-diagonals: 43,681,344
Integral-width: 1 Alphabet: 20 List-size: 50 CPU minutes: 5.25
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RESULT
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10 R22537 standard; Protein; 129 AA.
11 R2537 standard; Protein; 129 AA.
12 OJ-NOV-1997 (first entry)
12 OJ-NOV-1997 (first entry)
13 OJ-NOV-1997 (first entry)
14 OJ-NOV-1997 (first entry)
15 Warthody; 149th chain; variable region; hybridoma cell line 448104;
15 Warthody; 149th chain; variable region; hybridoma cell line 448104;
16 Warthody; 149th chain; variable region; hybridoma cell; line 448104;
17 Warthody; 149th chain; variable region; hybridoma cell;
18 Warthody; 149th chain;
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O4-JAN-1998 (first entry)
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TRY61. Single chain binding Single chain binding Single chain antibody D 12-3-37RY59 single chain antibody D 14-7 sc Anti-HYV-1 MD 447 sc Anti-HYV-1 MD 447
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peptide

Location/Qualifiers 118.133 /label= linker

09-70U-196: 09-70U-196: 09-70U-196: 09-70U-196: 06-FEE-1992: 831967. 06-FEE-1992: 08-31367. 07-00T-1993: 08-31367. 07-00T-1993: 08-31367. 07-00T-1993: 08-31367. 07-00T-1993: 08-313194.3. OPPORTMANN H, 18-00U-1901: 96-313134/3. OPPORTMANN H, 18-00U-1901: 96-313134/3.

Ring

8

ESULT 7

B W02280;

C W02280;

Z 39-00T-1996 (first entry)

E 35009 anti-c-erbb-1 wo single chain Pv construct.

W 53009; anti-c-erbb-2 monoclonal antibody; single chain Pv;

W construct; polymeride dibber; C-terminal antio acid seque

W in vivo imaging drug targetting experiment; bomodimer;

H in creased; binding avidity; tissue retention time.

Bomo amplens.

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The pref: vector or plasmid of the invention has a double-stranded the pref: vector or plasmid of the invention has a double-stranded try of the prefix of a variable region of a light or heavy chain of the production of the prefix of the prefix of the production of the prefix of the prefix of the prefix of the prefix of a variable region of a light chain having in the prefix of a variable region of a play of the prefix of th
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propsi standard; peptide; 146 MA.
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th 20.0%;
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29; Conservative
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/label= leader
23.130
/label= variable
131.146
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Pred. No. 9.98e-26;
0; Mismatches 0; Ind
                                                                                                                                          Score 29; DB 20; Le
Pred. No. 9.98e-26;
0; Mismatches 0;
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RESULT 11
D 127099; standard: Protein; 214 AA.
AC 427099; standard: Action of standard 
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C R39569:
C R39569:
C R39569:
D R Green of Sicc are protein "N-U, heterodimer; immunoglobulin; Ig:
D Sequence of Sicc are protein which the state of the protein of the state of the s
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25-ARF-1999; 303814.

21-ARF-1999; 305814.

21-ARF-1999; 105-184522.

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(EILI) ELI (Ally and Co.

Reservers LS. Bumol TF, Godski RA, Weigel BJ;

Reservers LS. Bumol Co.

Reservers LS. Bumol TF, Godski RA, Weigel BJ;

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Reservers L
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CC variable heavy (WH) and variable light (W1) sense were cloned from ca $2009 hybridona cDNA library, using probes directed troad the cc antibody constant and joining regions. A two single chain PY (PF) ce yene was constructed by connecting the W1 and W1 genes with PF (PF) ce yene was constructed by connecting the W1 and W1 genes with proceed to the present sequence, was inserted into an expression control to the culture medium. The standard of the W1 and W1 genes with the companion of carrier and the 2 sFy protein prod. can be affect in wive language, and drug targetting experiments. The case for in wive language as a monodium.

CC A compan, complains a carrier and the 2 sFy protein prod. can be compared to the wive language and drug targetting experiments arget the search products a homodium. In windows how for the search products a carrier and the CC longer times generation times, compared to individual sFy protein compared fragments execution times, compared to individual sFy protein sequence 243 AA;
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Best Local Similarity 100.0%;
Matches 28; Conservative
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3005;
-NAR-1990 (first entry)
ideric antibogy light chain variable region.
1/4: chimeric antibody; light chain variable region.
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Pred. No. 1.98e-24;
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RESULT 12

RESULT 12

RESULT 1895 standard; Protein; 216 AA.

AC #1595;

PM #
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Best Local Similarity 100.0%;
Matches 28; Conservative
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Match 20.0%;
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Matches 29; Conservative
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A single chain FV (gFV) is a covalently linked WFV hetroduler which is expressed from a gene fusion including VH and VL, encoding gene exponenced when a peptide-monoding linker. Such linker sequences are set forth in A residues 116-115 in R39569, which includes part of the 16 Au. linker sequences in R39572. Using 046084 for the 52059 monoclonal antibody, a single chain polypeptide can be produced having a binding affinity for a ceable 2 related antipon. X' in R39569 sequence 246 Au.
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Similarity 100.0%; Pred. No. 9.98e-26;
29; Conservative 0; Mismatches 0; Indels
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ed. No. 1.98e-24;

Mismatches 0;
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R75457; Standard: Protein; 218 AA.

R87 Primer; amplification: PR; mouse: Kappa Chain; heavy chain; Prb;

R8 Antibody: immunosolerance: animal; variequeted display library;

R8 Variable redion; antipen; immunosoceasive: cell surface; marker; foet

R8 cancer; stem cell; variant; therapy; Alebdaer's disease; hybridoms;

R8 cancer; stem cell; variant; therapy; Alebdaer's disease; hybridoms;

R8 cancer; stem cell; variant; binding affinity.

S8 kus musculus.

S9 kus musculus.

S9 binding 1995; U-154002.

S9 60-DE-1993; U-154002.

S9 60-DE-1993; U-154002.

S9 60-DE-1993; U-154002.

S9 60-DE-1993; U-15400.

S9 60
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Best Local S
Matches 2
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Best Local Similarity 100.0%;
Matches 28; Conservative
23-FEB-1992 (first entry)

single chain Fy from pSVVI for block
antigen-binding fragment: inflammati
Romo sapiems.

pr-155977-A.
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pp-155977-A.
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The present sequence represents the variable region of the third of antibody 362, produced by the hybridoma EAA362.
Sequence 216 AA;
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chain Fv from pSCV1 for blocking
chinding fragment; inflammation;
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Similarity 100.0%;
28; Conservative
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Pred. No. 1.98e-
O; Mismatches
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d. No. 1.98e-24:
Mismatches 0
      was able to protect cells against active than modified Fv fragments
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                                                                                                                                                                               f monoclonal antibody - can
to inter-cellular adhesion
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3. 1.98e-24;
--hes 0;
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auto-immune
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Query Match Best Local S Matches 2

h 19.3%; Similarity 100.0%; 28; Conservative

Score Pred. 0; }

re 28; DB 3; Ler 1. No. 1.98e-24; Mismatches 0;

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The sequence of the Light chain variable region from the mouse antibody 793-2. This sequence was isolated from a variegaced display library (VDL) 793-2. This sequence was isolated from a repertoke of antibodies from an expertoke of antibodies from a repertoke of antibodies from an expertoke of antibodies is the control of the primers of the control of the antibodies are used to construct an antibodies are used to construct an antibodies of the control of the antibodies produced antibodies produced by allows region and sensitive islands. The control of the antibodies produced between the control of the c
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Best Local S
Matches 2
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Mus masquist

MO$11581-X2.

15-UNN-1994; U1-106.

08-DEC-1994; U1-106.

08-DEC-1994; U3-1402.

06-DEC-1994; U3-1402.

DEC-1994; U3-1402.

DEC-1994; U3-1402.

DEC-1994; U3-1402.

MP-EDB: 09-2503.

WP-EDB: 09-2503.

WP-EDB: 09-2503.

WP-EDB: 09-2503.
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/5459 stance.
A75459:
O7-FEB-1996
Mouse antiborther: amy
which included a Gly-Gly-Gly-and H chains as either a monomer
see also RJ5437-RJ5442.
Sequence 240 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7-FED-1996 (first entry)
nuss antibody F4-7 light chain variable region protein sequence.
'imer: amplification; PCR; mouse; kappa chain; heavy chain; bary tibody; immnotoblerance; animal; variegated display library altriciable region; antigen; immnorecessive; cell surface marker; foetal; cer; etem cell; variant; therapy; Alzheimer's disease; hybridoma; musculus.

musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.3%;
Similarity 100.0%;
28; Conservative
                                                                                                                                                                                                                                          1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillhouse D.
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                                                                            -Ser flexible linker between
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09-JAN-1998 (first entry)
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R35959 (first entry)
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30-JUL-1997 (first entry)
Mouse anti-idiotypic antibody SA6 light chain variable region
Anti-idiotypic, anti-EGFR; epidermal growth factor receptor; tumour;
Concer: neoplasia; gloma; melanoma; carcinoma; drug manufacture; as
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R70828 standard: Protein; 154 AA.

AC 870828;

DE 1ANG-1995 (first entry)

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MA 6197X light (chain variable region.)

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204-DEC-1991.
04-DEC-1991.
01-JWN-1990. US-532001.
(HERY ) MERCE & CO INC.
COlono NJ. Confar NJ. Tomassini JE, Sardana VV;
A WPI; 91-35550/49.
A WPI; 91-35550/49.
TALCROBALLY expressed portions of monoclonal antibody can blocked attachment of Ininovirus ligands to inter-cellular adhesion per colonic (ICMA-1) per period of Measurements from Nab's specific for CC Ininovirus infection of Measurements from Nab's specific for CC Ininovirus infection See RISS7-1814() and to treat or proceedings of the Colonic Research (Nab's See RISS7-1814() Nable 134

18.61; Soure 27; DB 3; Length 124;
Pred. No. 3 88e-23; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
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           100
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Score
Pred
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Pred.

re 27; DB 22; Ler d. No. 3.88e-23; Mismatches 0;

Length 143;

Indels

0

Gaps

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124 141

's specific for domain

block

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No.

DB 13; 3.88e-23;

Length 154

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Apr
19 13:23:51
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XOD

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127
            27;
            Conservative
                     .:..
            9
153
              Mismatches
                       US-08-836-455-2.rag
              <u>..</u>
              ő
              Gaps
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Apr 19 13:23:51 1999

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RI1286 standard: Protein: 108 AA.
RI1286 tandard: Protein: a\*, apecific for phox.
Rurine VL Rappa group V chain \*a\*, apecific for phox.
Rurine VL Rappa group V chain \*a\*, apecific phagenid: capation: phina: phin

Query Match 18.6%; Best Local Similarity 100.0%; Matches 27; Conservative

Pred.

e 27; DB 8; Length I. No. 3.88e-23; Mismatches 0; Ind

225;

0

therapeutic agents Sequence 225 AA;

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email
cytotoxic agent.
Rey
                                                                                                                                                                        region
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40385
40385
8-FEB
onocl
                                                                                                                                                                                                                                              standard; Protein;
                                                                                                                                                                                                                artibody M(alpha)2-3 light-chain.
antibody M(alpha)2-3 light-chain.
amall neurotoxin antibody; kappa; light chain;
amall neurotoxin antibody; cell-targetting;
amall bispecific bivalent antibody; cell-targetting;
                                                                                                                                                                   Location/Qualifiers
1. 12
/label= signal_peptide
13. 11
/label= variable
/label= constant
/label= constant
                                                                                                                                                                                                                                              225 AA.
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binding\_site

Location/Qualifiers
24.34
74.34
71abel= CDR1
50.56
71abel= CDR2
89.96
71abel= CDR3
7note= D-X-G-X-X mo

CDR3 D-X-G-X-X motif \*

binding\_site

We would not be with a secreting replicable genetic for the Yapronces a diverse reperiors of antique genetic for yapronces a diverse reperiors of antiques. Corporate a diverse a diverse a diverse a diverse description of the yapronces and the property of the production seems of a pecific binding pairs - by expression in producing members of apecific binding pairs - by expression in producing members of apecific binding pairs - by expression in producing members of apecific binding pairs - by expression in producing members of a pecific binding pairs - by expression in producing members of a pecific binding pairs - by expression in producing members of a pecific binding pairs - by expression in producing members of a pecific binding pairs - by expression in producing members of a pecific binding pairs - by expression in producing members of a pecific producing a diverse reperiors of antibody frequents apecific for Example 11: Fig 24: 209py. English

CC Typendy-5-oxarolone (phoz). It was prept. using cDNA generated control of the producing members and producing cDNA generated control of the producing control of the p

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19
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ce from mBMA from make immunised with phox coupled to chloked serum ce albumin for YN and VL kappa sequences were speakesty amplified by president on the phage surface as fusions with gene 137457 lore except president to the phage surface as fusions with gene 11. The resultance of clones were sequenced revealing sight different VN genes (A-H) (see CR21264-71) in a variety of pairings with the seven different VR created to the control of 
See also R21260-307, 309-311; R22450,
Sequence 108 AA;
                                                                                                           565-501.
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88888888888888888888

Query Match Best Local S Matches 2 0 Length 108; Indels 0 Caps

ő

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RESULT 32
RESULT 193 (first entry)
RESULT 193
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t which are

ilon receptors - act as preventing IgE-mediated

. zag

17.9%; Similarity 100.0%; 26; Conservative Score Pred. re 26; DB 4; L f. No. 7.53e-22; Mismatches 0

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1999

នននននន substantially incapable of binding PCEH-bound 1gE listantine release from mast cells or basophils, on Kabat CDR docaln into which has been substituted analogous residue from a Rabat CDR domain of the antibodies Walli, MREIJ, MREIS or NATI?

IgE or inducing , comprise a human ed a positionally he murine anti-huigE

Query Match 17.9%; Best Local Similarity 100.0%; Matches 26; Conservative Score Pred. re 26; DB 6; d. No. 7.53e; Mismatches , DB 6; Leuy , 7.53e-22; -hes 0; Length 124; 0

**5** \$

0

RESULTANT OF STATE OF 127 24
R15322 standard: Protein; 144 AA.
R15322; standard: Protein; 144 AA.
16-MAR-1992 (first entry)
16-MAR-1992 (first entry)
11C-2 chimeric entribody light chain.
Interiekin-12 immunosuppressant.
Chimeric Hom daplens.
Chimeric Hom daplens.
Chimeric Hom daplens.

Key peptide peptide Location/Qualifiers
Location/Qualifiers
Potes
11:115 signal peptide\*
11:115 v-region\*
11:00:14
10:14:171-region\*
10:14:171-region\*

peptide peptide

PH pp-46674-A. /hote\* "C-region"

PH pp-46674-A. /hote\* "C-region"

PH pp 11-D2-1991.

PP 60-TM-1991. D99101.

PP 60-TM-1990. DF-018442.

PH 6027 | DoBRINGER MANNIEIM GABH.

Reicht (, Kaluna B. Knapp H;

PH 9709; (Jill4 )

PH PD (Jill4 )

PH PD (Jill4 )

PH PD (Jill4 )

PH Net Prochainant DNA encoding chimeric antibody - with human receptors are receptors.

PH Net Prochainant DNA encoding chimeric antibody - with human receptors.

PH Net Prochainant DNA encoding chimeric antibody chimeric antibody of the chimeric antibody of the chimeric antibody come uneful a immunogenerator, and order antibody come or ret antibodies. See also N19121-R15136.

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Mon
        Apr 19 13:23:51
        1999
US-08-836-455-2.rag
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ដ្ឋដូច្រក្សត្តិ

Monoclonal anti-dictypic antibodies misicking epidermal growth factor receptor - useful for twoor therapy Claim 6; Fig 5b; 28p; English can thooler, 1880, 386 and 586 are new They induce an immune reponse against epidermal growth factor receptor (RERS). The accurace are given in the specification. The antibodies are used for the manufacture of drugs directed against through that express EGFR on their surface, including melanomas, Sequence 146 AA;

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문
                            Query Match 17.9%;
Best Local Similarity 100.0%;
Matches 26; Conservative
Score 26; DB 3;
Pred. No. 7.53e-
0; Mismatches
                         DB 3; Le.,
7.53e-22;
                                        Length 144;
                            0
                            Caps
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region peptide

**8** 8

141 144 Query Match Best Local S Matches 2

h 17.9%; Similarity 100.0%; 26; Conservative

Score Pred. 0;

re 26; DB 22; Ler d. No. 7.53e-22; Mismatches 0;

Length 146;

Indels

0

region region region

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EP-145612-A1. JULES BOURSE CO. 104-DEC-1996. 107631. 14-DEC-1996. 107631. 26-DEC-1997. 26-DEC-1997. 26-DEC-1997. 26-DEC-1997. 26-DEC-1997. 26-DEC-1997. 36-DEC-1997. 36-DEC-19
                                                                                                                                                                                                                                                                                                                                                                 Piulats J,
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19

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US-08-836-455-2.rag

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determining region
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VISTO 28 standard: Protein; 146 AA.
VISTO 38 standard: Protein; 146 AA.
VISTO 30-7UL-1997 (first entry)
10-7UL-1997 (first entry)
Mouse anti-4diotypic antibody 386 light chain variable region.
Anti-4diotypic, anti-5gr; epidermal growth factor receptor; tumo
kancer: neoplasia; 910mm; melanoma; carcinoma; drug manufacture;
Mouse masculist.
region
                                                                                                                                                        region
                                                                                                     2.
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region region

REAL SAME CONTRACTOR OF THE SECOND SE

14-MAR-1990 (first entry)
Light chain of monoclonal antibody 6A4.
Monoclonal antibody 6A4; light chain; Pseudomonas

standard; peptide; 148

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ph 13-NPR-1985; 106463.

PR (12ENP) Behingwerte

Pr (1

67.4 and

2

Mon Apr 19 13:23:51 1999

US-08-836-455-2.

Fag

8 B

Query Match 17.9%; Best Local Similarity 100.0%; Matches 26; Conservative

; Score 26; DB 1; ; Pred. No. 7.53e-0; Mismatches

DB 1; Length 148; 7.53e-22; atches 0; Indels

0

Gaps

Page

5

នឧឧឧឧ cells and growth of ICM-1 expressing tumour cells, to treat viral infection to suppress extravacular migration of virally infected leucocytes and to treat asthma.

See also R15300.
Sequence 172 Ak;

Query Match Best Local s Matches 2 h 17.9%; Similarity 100.0%; 26; Conservative Score 26; DB 3 Pred. No. 7.53e 0; Mismatches 9 Length 172; Indels 0 Gaps

0

8 B 

region region region peptide 72 28
RL5059 standard; Protein; 173 AA.
RL5059 standard; Protein; 173 AA.
RL5059 standard; Protein; 173 AA.
Hurine anti-TCAH monoclonal antibody light chain.
Hurine anti-TCAH monoclonal antibody light chain.
Hurine cellular adheafon molecule; variable region; V(L);
R6-5-06 murine MAD; complementarity determining region;
R6-5-06 murine MAD; complementarity determining region;
Key Location/Qualifiers /label= leader
43.58
/label= CDR1
74.80
/label= CDR2
113.121
/label= CDR3
/label= CDR3 Location/Qualifiers 1..19

region

region region region

Location/Qualifiers
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Ligion/Qualifiers
Location/Qualifiers
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\*confirmed by N-terminal

peptide

RI5199 stands
RI5199;
14-FEB-1992
R6-5-D6 antiIntercellular
Hus musculus
Key
peptide

(first entry) -ICAM-1 light chain. r adhesion molecule-1; antibody;

standard;

Protein; 172

3

Pr No9116928-A.

Pi 14 : NOV-1991.

PD 14 : NOV-1991.

PD 25 - APR-1991 | D02946.

PP 27 - APR-1991 | GB-009548.

PP 27 - APR-1991 | GB-009548.

PP 28 - APR-1991 | GB-009548.

PP 29 - APR-1991 | GB-009548.

PP 20 - APR-1991 | GB-009548.

PP 30 : APR-1991 | GB-009548.

PP 40 : APR-1991 | APR-1992 | APR-1992

Woolise27-A.

AADea constant

BY ANDV-1991

domain

constant

Page 48

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profit Str. 1996.

Profit Profit Str. 1996.

Profit Profit Profit Str. 1997.

Profit Profit Profit Str. 1997.

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                                                                                          Example: Figure 2: 42pp: English.

Exhibit: Figure 2: 42pp: English.

Exhibit: As proped, from procedual intellectory call line (162/86) which may be apped and procedual for the first procedual for first procedual for the superior sequence deduced (65449/R4444). The sequences of a partial kappa clone (kappa-4ACl) which encoded the trained in a similar fashion. To determine deduced (65449/R4444). The sequences of a partial kappa clone (kappa-4ACl) which encoded the trained in a similar fashion. To determine the sequence of the collection for the first procedual for the first p
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Matches 2
       Query Ma
Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
W03124610-A.

09-DEC-1993.
19-HAY-1993. R100228.
12-HAY-1992. R100251.
(AGEN-) ACEN LTD.
Hillyard CCJ. Hudson PJ. Li
Hillyard CCJ. Hudson PJ.
Hillyard CCJ. Bidson PJ.
WPJ: 93-405801,50.
Bidunctional recombinant pro
binding moieties, used in ag
blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 29
R1593] standard: Protein: 214 AA.
R1593] standard: Protein: 214 AA.
R1593] (first entry)
09-DEC-1997 (first entry)
Antibody 7021 light chain variable region.
catalytic antibody; enantioselective hydrolysis;
EAN7012: EAN302; da.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 murine framework-encoding sequences (i.e. not encoding CDRs) will be replaced by human framework sequences to produce recombinant (CDR-grafted humanised) antibody molecules having specificity for ICNN-1. Sequence 173 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 13:23:51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents the variable region of antibody 7G12, produced by the hybridoma ZAA7G12. Sequence 214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_difference
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war: 194 (first entry)
genoe of the immunoglobulin 196 (163/86) kappa chain
tived from close gammal. Lia and augmented using PCR.
ticle-binding antibody fragment; kappa chain;
potional cell line 163/86; anti-erythrocyte 196s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein;
h 17.9%;
Similarity 100.0%;
26; Conservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 17.9%;
Similarity 100.0%;
26; Conservative
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213
/note= "encoded by '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein - contains particle
agglutination assays pref.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lilley
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0; Mismatches
       Pred. No. 7.53e-22
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1, 7,53e-22;
1-8 0;
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                                                 Length
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       ngth 219;
Indels
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Query Match Best Local S Matches 2

h 17.9%; Similarity 100.0%; 26; Conservative

Score 26; DB 23; Le Pred. No. 7.53e-22; 0; Mismatches 0;

Length 222;

Indels ္ပ

Gaps

0

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S.
               22 AA.

27 21-AXC-1997 (first entry)
28 Mil monoclonal antibody Azppa chain,
W CDR; light chain; antigen bidding site; antigen free
KW germires anthall; immunoreactive; thrombotic event.
S Mus musculus.
Location/Qualifier*
T domain 19 %
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
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PH W09640986-A1.

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PD 06 JUL-1934: GO2610.

PR 07-MOV-1944: GO2610.

PR 07-MOV-1944: GO2610.

PR 07-MOV-1944: GO-210.

PR 0
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Best Local Similarity 100.0%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
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Ab 55.1 light chain.

Trigen blinding structure; complementarity determining region;

A55.1 colorectal cancer; tumor-sesociated antigen; hybridoma;

A55.1 colorectal cancer; tumor-sesociated antigen; hybridoma;

associant antibody; Abb. immunotherapy; therapy diagnosis;

resegmic entantibody; immunotherapy; therapy diagnosis;

use and tumorized antibody; immunotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13:23:51
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Pred. No. 7.53e-22;
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ph top 722599-A2. /Note complementarity determining region 3. pp 16-JUN-1987. 20075; pp 19-DEC-1987. 20075; pp 19-DEC-1987. 20075; pp 19-DEC-1985. 20075; pp 19-DEC-1985. 20075; pp 20-DEC-1985. US-572762. pp 20-DEC-1985. US-572762. pp 26-JUN-1985. US-572762. pp 26-JUN-1985. US-572762. pp 26-JUN-1985. US-572762. pp 27-JUN-1985. US-572762. pp 27-
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by woo500013.4.

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24.34
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Pred. No. 7.53e-
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d. No. 1.45e-20;
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RESULT 37

ID R99686 standard: Protein; 142 AA.

C 89686; Respective to the standard of the st
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DT 27-App.

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pp 11-APR-1997; 00583.

pp 10-APR-1997; 00583.

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pp 10-APR-1997; 00583.

pp 10-APR-1997; 00583.

pp 10-APR-1996; 09581005.

pp 10-APR-1996; 09581005.

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ID W27121 standard;
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Anti-1dotype antibody 3H2; carcino
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R76087 standard; Protein; 239 AA.
R76087, standard; Protein; 239 AA.
R76087, standard; Protein; 239 AA.
R76087, standard; charter; prophementarity determining regilated antigen binding structure; complementarity determining regilated. CASS.1. colorestA. cancer; tumor easociated antigen; hybrid monocloral antibody; Mybrid immunoteaeapy; therapy; diagnosis transgenic antibody engineering; when an antibody engineering when any engineering when any engineering engineering when any engineering engineering engineering when an antibody engineering e
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Similarity 100.0%;
25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1.20
/label= Sig_peptide
21.239
/label= Mat_protein
/note= "claim 3, page 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
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0; }
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ed. No. 1.45e-20;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ζ
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incembryonic antigen; CEA;
colorectal cancer; lung cancer;
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Length 239;

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Gaps

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Length 142;

Indels

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Gaps

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71..108 /label= Framework-3 109.127 /label= CDR3 128.142 /label= Framework-4

SN WHOSO 11-A2.

SN WHO

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Score 25; DB 18; L Pred, No. 1.45e-20; 0; Mismatches 0; Length 142

Query Match 17.2%; Best Local Similarity 100.0%; Matches 25; Conservative 142

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Gaps

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High 38 anndard; Protein; 142 AA.
R99410 standard; Protein; 142 AA.
R99410 standard; Protein; 142 AA.
R99410 standard; Protein; 142 AA.
18-SEP-1996 (first entry)
Hilight Chain wariable region.
Anti-14docype; monoclonal antibody; MAD; 3H1; CEA;
A carcinosmiryontic antisen; cancer; gene therapy; in
vaccine; genetic immunisation; light chain; VL.
V.--nn Mus sp. Key region region region Location/Qualifiers
21.32
/label= Framework-1
44.54
/label= CDR1
55.69
/label= Framework-2
70.76
/label= CDR2 CEA; y: immunotherapy;

/note=

Processing the process of the proces

Query Match Best Local S Matches 2 h 17.2%; Similarity 100.0%; 25; Conservative ; Score 25; DB 28 ; Pred. No. 1.45e-O; Mismatches ມ8 28; `.45e-20; \*\*s 0; Length 238; Indels 0

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RESULT. 39
IN WAINES tendard: Protein; 238 AA.

AC WAINES.

DY 15-ARR-1998 (first entry)
DY 15-ARR-1998

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Query Match Best Local S Matches 2

h Similarity 100.0%; 25; Conservative

Score Pred. 0; }

re 25; DB 18; Le: d. No. 1.45e-20; Mismatches 0;

Length 142; Indels

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complementarity determining \*framework region 2\* complementarity determining

\*framework region \*complementarity determining \*framework region 3\* è

Region

Region

Region

Property of the firemework region 4° prior protein - used for prior 1-22-136; US-53104.

Prince - 1997. US-53104.

Prince - 1997. OLIFORNIA.

Prince - 1997.

Query Match 16.6%; Best Local Similarity 100.0%; Matches 24; Conservative 99 65

Score 24; DB 25; L. Pred. No. 2.75e-19; O; Mismatches O;

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Query Match Best Local & Matches

h 15.2%; Similarity 100.0%; 22; Conservative

Pred.

re 22; DB 10; Len d. No. 9.52e-17; Mismatches 0;

142 128

SEUT 43
SEUT 43
SEUT 43
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SECTION 125
SECTION 125
Anti-tobacco mosaic virus monocional ab
robacco mosaic virus TRY; monocional ab
119h chain: virus-restant plants; bi
synthetic.
Location/Qualifiers
peptide 1.20
Location/Qualifiers
Location/Qualifiers
Location/Qualifiers
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Location/Qualifiers

l Ab light chall antibody; biofarming.

J06319396-A 22-NOV-1994

domain peptide

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7.00te= "constant K domain"

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DESULT:

10. 1033573 standard: Protein: 667: AA.

21. 1033573 standard: Protein: 667: AA.

22. 1037573 standard: Protein: 667: AA.

23. 2037573 standard: Protein: 667: AA.

24. 2037573 standard: Protein: 667: AA.

25. 2037573 standard: Protein: 667: AA.

26. 2037573 standard: Protein: 667: AA.

27. 2037573 standard: Protein: 667: AA.

28. 2037573 standard: Protein: 667: AA.

29. 2037573 standard: Protein: 667: AA.

29. 2037573 standard: Protein: 667: AA.

2037573 standard: Protein: 667: AA.

203757 standard: Protein: 667: AA.

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PR (NISS) JAPAN TORACCO INC.

PA (NISS) STRUMAY COLOR INC.

PA (NISS) S
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ID 83902 standard; Protein; 220 AA.

AC 83902;

AC 83902;

PA 131-DE-1994 (first entry)

DE FAB 113pht chain for 1McP.

EN McPc603; V-min; synthetic gene; Dl.3; antibody; immunotoxins; tumour;

EN McPc603; V-min; synthetic gene; Dl.3; antibody; immunotoxins; tumour;

EN intracellular expression; B. coli; protease deficient; treatment;

EN 119nd-binding variable domain; framework region; beca-barrel;

EN 119nd-binding variable domain; framework region; beca-barrel;

EN beta-sheet; linker; complementarity determining regions; radioimaging;
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PF Humanised antibody specific for select sub-population of T cells

PF Humanised antibody specific for select sub-population of T cells

PT useful for treatment of Cobbin of select and Multiple Sclerosis

PT useful for treatment of Cobbin discretion for the formation of the
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Synthetic,
W09516018-A,
15-UUN-1995, IB0387.
21-NOV-1999; GB-025182.
(NERC) MERCER C P.
(MERC) T CELL SCI INC.
1-14n AV:
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177307 etandard, peptide; 153 AA.
177307;
177307;
13-NOV-1995 (first entry)
13-NOV-1995 (first entry)
10-80 light chain sequence
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Similarity 100.0%;
22; Conservative
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Pred. No. 9.52e-17;
0; Mismatches 0;
                       ifgen expressed on the surface of ovarian tumour cells, which is an glycoprotein having an isolelectric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               re 22; DB 13; Ler
d. No. 9.52e-17;
Mismatches 0;
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                                                                       δ β.
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CC is a covalently linked WT. The terodiser which is expressed from
CC a spen dissinctly linked WT. The first produce of the secondary linke WT. The first produce of the secondary linke WT. The secondary linke WT. The secondary linke WT. The secondary linker sequences are set forth in
CC initiate sequences in $3973958, which includes part of the 16 AA
CC antibody, a single chain years price can be produced having a
CC the pseudomonal excitation for a crebal price can be produced having a
CC the pseudomonal excitating for a crebal produced having a control of the secondary terminus of Alogous to ricin A chain, p840,
CC in fued to the carboxy terminus of Alogous to ricin A chain, p840,
CC the resulting 741F8 sPv-P840 is a chips anticoverbs 2711 sPv.
CC protein, which was constructed with an chain Pv-routh fusion
CC which initially was left on the protein. X in R39573 refers to
CC Sequence 657 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       នួននួននួននួននួននួននួន
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Best Local S
Matches 2
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Query Match Best Local Similarity

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sh 15.2%; Similarity 100.0%; 22; Conservative

Pred. 257

22; DB 8; Length No. 9.52e-17; Mismatches 0; Ind

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Chaim 6; Fig 59; 28pp; English.
Murine monoclonal anti-idiotypic antibodies, 1598, 386 and 586 are
new. They induce an immune response against epidermal growth factor
receptor (EEFR). The sequences of the heavy and light chain variable
respons of these antibodies are given in the specification. The
antibodies are used for the manufacture of drugs directed against
tumours that express EEFR on their surface, including melanomas,
glionas and carcinomas.
                                                                                                                                                                                                                                                                                                                                                                 19 13:23:51
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Score 21; DB 22; LA Pred. No. 1.73e-15; 0; Mismatches 0;

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The Residence of the state of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-745612-A1. Indication of the control of the cont
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30-JUL-1997 (first entry)
Mouse anti-idiotypic anti-BoFR; epidermal
Anti-idiotypic; anti-BoFR; epidermal
cancer; neoplasia; glioma; melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13:23:51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 13.8%;
similarity 100.0%;
20; Conservative
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IN R8972 standard; Protein; 107 AA.

MC R18972 standard; Protein; 107 an antibody 586.

MC R18972 standard; Protein; 107 an antibody 586.

MC R2972 standard; 107 an antibody; heavy metal; mercury; variable region;

MR 11972 standard; 1070.

MR 11972 standard; 1070.

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bind heavy metals, esp. mercury - derived from sed for detecting, removing, adding or

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ogunidine isothicognante, First strand cDNA synthesis was catalysed by Milx process transcriptase. The princes used for cDNA synthesis was catalysed were complementary to the 5 and of the CHI domain of the heavy of the chine expressed by the hybridoms of interest, or to the 5' and of the chine princest of the the 5' and of the chine princest of the princest of the solven in 07511-097518. The princest used for cDNA synthesis of the catalyst region of a particular antibody polypeptide was also used of PRA supplification of that watable region, in conjunction with the appropriate v-region princes. In addition, the Wiprimer 097518 or a superior to amplify the mbb 25b and 586 heavy chains. The sequences of the PRA supplified nucleotides were determined. These are given to 199749997310 and the deduced An sequence on RF3941-RF9350 at 19974997310 and the deduced An sequence on RF3941-RF9350 at 19974997310 and deferring the descriptions of the sequence listings. The descriptions in the sequence listings are caused here 1974 As 1974

Sequence 107 AA; Match 13.8%;
Local Similarity 100.0%;
les 20; Conservative Pred. re 20; DB 14; Ler d. No. 3.10e-14; Mismatches 0; Indels 0 Gaps

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ESSUIZ.

RE 19247; standard; Protein; 107 AA.

R 19348; standard; protein; 107 AA.

R 193520607; A.

R 19352007; A.

R 193520607; A.

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pharmacology, medicine and blochemical fields.

Exampla 5, 2ege 22; 2mpy, Japanese
R74960-R74969 are clones of the anti-idiotype antibodies idio3, Idio17,
Idio20, Idio27 and Idio33 against a human anticancer memoconal antibody.
These antibodies and DNA emodding them are useful in pharmacological,
medical and boochemical fields of research.
Sequence 120 AA;

5 B Outry March 13.8%; Score 20; DB 14; Length 120; Best Local Similarity 100.0%; Prod. No. 3.10e-14; Marches 20; Conservative 0; Mismatches 0; Indels 0; Gaps

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Search completed: Thu Apr 15 18:07:59 1999 Job time: 94 secs.

ð å Shamoryanin (RLH). Eight hybridomas (1910. 4A10, 1011. 564, 2378, 205, CC against distrate producing Mobas that were strongly ipositive considered that the strong of the 888888888888888888888888 Ouery Match 13.8%; Score 20; DB 14; Length 107; Best Local Similarity 100.0%; Pred. No. 3.10e-14; Matches 20; Conservative 0; Mismatches 0; Indels 0; Location/Qualifiers
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                                                                                                            Apr 19 13:23:53 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 77148916.
BURSTEIN Y., SCHECHTER
PROC. NATL. ACAD. SCI.
                                                                                      GUINOGLOBULIN V REGION: SIGNAL; BENCE-JONES PROTEIN.

GUNAL 23 116 JG KAPPA, CHAIN V-V REGION (
MAIN 24 45 PRAMEMORE N

MAIN 46 56 CONPLEMENTARITY-DETERMINING

MAIN 77 70 FRAMEMORE N

MAIN 72 70 CONPLEMENTARITY-DETERMINING

MAIN 72 10 CONPLEMENTARITY-DETERMINING

MAIN 72 110 CONPLEMENTARITY-DETERMINING

MAIN 101 110 CONPLEMENTARITY-DETERMINING

MAIN 101 110 CONPLEMENTARITY-DETERMINING

MAIN 101 120 PRAMEMORE N

MAIN 102 120 PRAMEMORE N

MAIN 104 120 PRAMEMORE N

MAIN 105 110 CONPLEMENTARITY-DETERMINING

MAIN 105 110 CONPLEMENTARITY-

MUTUAL 110 CONPLEMENTARITY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I.;
U.S.A. 74:716-720(1977).
                                                                                                                                                IG KAPPA CHAIN V-V REGION (MOPC 41).

PRAMEMORIK 1.

PRAMEMORIK 2.

PRAMEMORIK 2.

COMPLEMENTARITY-DETERMINING 2.

PRAMEMORIK 3.

COMPLEMENTARITY-DETERMINING 3.

PRAMEMORIK 4.

PRAMEMORIK 4.
                                                                               E77D75A2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-836-455-2.rsp
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ş 문 Query Match Best Local s Matches 2 b 20.0%; Similarity 100.0%; 29; Conservative Score 29; DB 1; Les Pred. No. 1.46e-57; 0; Mismatches 0; Length 130 Indels

.;

Gaps

0

RESULTS

10 NOVE STANDARD; PRT; 117 AA.

10 POIGLIOUSE STANDARD; PRT; 117 AA.

11 POIGLIOSE STANDARD; PRT; 117 AA.

12 11-UL-1986 (REL. 01, CREATED)

12 1-UL-1986 (REL. 01, LAST REMOVERCE UPDATE)

13 11-UL-1986 (REL. 01, LAST REMOVERCE UPDATE)

14 12 12 13 NOVERCE AL LAST REMOVERCE UPDATE)

15 14 APPA CHAIR PRECUENCE (NOVERCE)

16 14 PAPA CHAIR PRECUENCE (NOVERCE)

17 14 PRECUENCE (NOVERCE)

18 12 14 PRECUENCE PROW N.A.

18 12 14 PRECUENCE PROW N.A.

18 14 15 PRECUENCE PROW N.A.

18 15 PRECUENCE PROW N.A.

18 16 PRECUENCE PROW N.A.

18 16 PRECUENCE PROW N.A.

18 17 PRECUENCE PROW N.A.

18 18 PRECUENCE PROW N.A. SEQUENCE FROM N.A. MEDLINE: 81064681. MAX E.E., SEIDMAN J.G., MILLER H., LEDER P.; MAMMALIA;

RESULT ACCORDED TO THE PROPERTY OF THE PROPERT

SEQUENCE FROM N.A.
MEDLINE; 79221900.
SEIDMAN J.G., MAX E.E.,
NATURE 280:370-375(1979) SEQUENCE OF 1-33

POLGAN POLGAD.

21-UUL-1986 (REL. 01, CRAATED)
21-UUL-1986 (REL. 02, CRAATED)
01-CUT-1996 (REL. 03, LAST SEQUENCE UPDATE)
01-CUT-1996 (REL. 03, LAST ANNOTATION UPDATE)
UG ANDRA CHAÍN PROCURSON V-V RECIDON (MODE 41).
HIS MISCULAS MODENTA.
EUTHARTON, METAMON, CHORDATA; VERTEBRATA; TETRAFODA; MAMALIA;
111 HERIA, MODENTIA.

STANDARD;

PRT:

130 AA.

ALIGNMENTS

Apr US-08-836-455-2.rsp

Query Match Best Local S Matches 1 similarity 100.0%; 16; Conservative Score 16; DB 1; Length 117; Pred. No. 2.64e-21; 0; Mismatches 0; Indels .. Gaps 0

IN ESULT 4

A 6 90431.
AC 90431.
AC 904331.
AC 905.
AC IRANDA CHAIN V-I REGION (WALKER).
FRANDORS, 1.
FRANDORS, 2.
FRANDORS, 2.
FRANDORS, 2.
FRANDORS, 2.
FRANDORS, 2.
FRANDORS, 2.
COMPLEMENTARITY-DETERMINING 2.
COMPLEMENTARITY-DETERMINING 3.

19 13:23:53 1999

Page

2

12799 MW; B02D3EA1 CRC32;

В 8 21 RCDIQMTQSPSSLSAS 36

RESULT 1

AC POLGOU STANDARD; PRT; 117 AA.

DT 21-JUL-1986 (REL. 01, CREATED)

DT 01-AVX-1996 (REL. 01, LAST ANDONATION UPDATE),

DT 01-AVX-1996 (REL. 18, LAST ANDONATION UPDATE),

DE 1G KAPPA CHAIN PRECONSOR V-I REGION (HAIO1) (FRAGMENT).

OC EUTHRATO-N. HETALON, CHORDATM, VERTEBRATM; TETRAPODA; MAMMALIA;

RESIDENCE FROM N.

R

Ş 밁

Query Match 12.4%; Best Local Similarity 100.0%; Matches 18; Conservative

Score 18: DB 1; Length 117; Pred. No. 1.34e-26; 0; Mismatches 0; Indels

0

Caps

0

38F2B08C CRC32;

STATETETETERS

V REGION: SIGNAL.

117 IG K.
127 IG K.
45 FRAMAL
56 COMP.
78 COMP.
110 PRAM.
2117 COMP.
110 BY S:
AA: 11954 MW; 388

IG RAPPA CHAIN V-V RECION (MOPC 17
PRANEMORK 1.
COMPLEMENTARITY-DETERMINING 1.
PRAMEMORK 2.
COMPLEMENTARITY-DETERMINING 2.
PRAMEMORK 3.
COMPLEMENTARITY-DETERMINING 3.
BY SIMILARITY.

173B)

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Apr 19 13:23:53 1999
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8333

DOMAIN 120 1 DISULFID 45 1 NON\_TER 129 1 SEQUENCE 129 AA;

129 PRAMEWORK 4. 110 BY SIMILARITY. 129 14069 MW; 99925172 CRC32;

Query Match 11.0%; Best Local Similarity 100.0%; Matches 16; Conservative

US-08-836-455-2.rsp

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Mon

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PIR: A02119; KIMS.
PIR: $01320; $01320;
HSSP; PO1842; 15AP.
HSSP; PO1842; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KYLO_UTUAN STANDARD: PRT: 108 AA.
12.UUL-196 (REL. 01, CREATED)
21.-UUL-196 (REL. 01, ARS EBQUENCE UPDATE)
21.-UUL-198 (REL. 01, ARS EBQUENCE UPDATE)
10.-ANN-1988 (REL. 02, LAST ANNOTATION UPDATE)
10.-ANN-1988 (REL. 03, CHORDATA; VERTEBRATA; TETRAPODA: MAMALIA;
10.000 SAPIENS (HUMAN); CHORDATA; VERTEBRATA; TETRAPODA: MAMALIA;
10.000 SAPIENS (HUMAN); CHORDATA; VERTEBRATA; TETRAPODA; MAMALIA;
10.000 SAPIENS (HUMAN); CHORDATA; CHOR
                                                                                                                                                                                                                           COMPLEMENTARITY-DEFERMINING 1.
ENAMEMORE 2.
COMPLEMENTARITY-DEFERMINING 2.
FRANCHORM AND DEFERMINING 3.
FRANCHORM 1.
BY SHILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16: DB 1: Length 129: Pred. No. 2.64e-21: 0; Mismatches 0; Indels 0;
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A HEDLING: 75059112.

A HEDLING: 75059112.

A HAURE C.J., WATNABE S., HILSCHARN N.;

A HOPPE-SEYLER'S Z. PHTSICK. CHEM. 554:150-1504(1973).

CC 1: THE CRESION OF THIS CHAIN HAS THE INV (3) MARKER.

CC 1: THE CRESION OF THIS CHAIN HAS THE W (3) MARKER.

CC 1: THE CRESION OF THIS CHAIN HAS THE PROBLEM TO THE ADMINISTRATION OF THE 
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RESULT 9
ID KVIA_HUMAN
AC PO1593;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.7%;
Best Local Similarity 100.0%;
Matches 14; Conservative
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Matches 14; Conservative
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PD1559;
21.-UL-1986 (REL. 01, CREATED)
21.-UL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01.-UAR-1986 (REL. 05, LAST ANOTATION UPDATE)
10.-UAR-1986 (REL. 05, LAST ANOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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MOSES STANDARD; PRT; 106 AA.

PO1817.

11-UUL-1986 (REL. 01 LOREATED)

11-UUL-1986 (REL. 01 LAST SEQUENCE UPDATE)

10-CUT-1986 (REL. 14, LAST ANNOTATION UPDATE)

10 NOT-1986 (REL. 14, LAST ANNOTATION UPDATE)

10 NOT-1984 (REL. 14, LAST ANNOTATION UPDATE)

11 NOT-1984 (REL. 14, LAST ANNOTATION UPDATE)

12 NOT-1984 (REL. 14, LAST ANNOTATION UPDATE)

13 NOT-1984 (REL. 14, LAST ANNOTATION UPDATE)

14 NOT-1984 (REL. 14, LAST ANNOTATION UPDATE)

15 NOT-1984 (REL. 14, LAST ANNOTATION UPDATE)

15 NOT-1984 (REL. 14, LAST ANNOTATION UPDATE)

16 NOT-1984 (REL. 14, LAST ANNOTATION UPDATE)

17 NOT-1984 (REL. 14, LAST ANNOTATION UPDATE)

18 NOT-1984 (REL. 14, LAST ANNOTATION UPDATE)

18 NOT-1984 (REL. 14, LAST ANNOTATION UPDATE)

19 NOT-1984 (REL. 14, LAST ANNOTATION UPDATE)

19 NOT-1984 (REL. 14, LAST ANNOTATION UPDATE)

10 NOT-1984 (REL. 14, LAST ANNOTATION UPDATE)
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MEDLINE, 81191915.
MAX E.E., 811812TL J.V. JR., LEDER P.;
J., BIOL. CHEM. 256:5116-5120(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEDERICE PROM N.A.
DE MARIE 9833981.
DE MARIE P., PETS V., VAN DE VOORDE A., MOLEMANS F., FIERS W.;
ENDR. U. BICCIEM. 176:88-295(1988).
ENDR: VOORD7; 623133; -.
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EDLINE; 81198949:
LTEMBURGER W., NEUWAIER P.S., STEINMETS M.,
VOLEIC ACIDS RES. 9:971-981(1981).
                                                                                                                                                                                                                                                                                    1 DIGMTQSPSSLSAS 14
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EDLINE; 82059477.
MALYN P.H., GAIT M.J., MILSTEIN C.;
PULEIC ACIDS RES. 9:4485-4494(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQUENCE (MOPC 21).
EDLINE: 73053310.
VASTI J., MILSTEIN C.;
VASTI J. 128:427-444(1972).
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DIINE: 79084137.
MILYN P.H., BROWNIES G.G., CHENG C.-C., GAIT N.J., MILSTEIN C.:
LL 15:1067-1075(1978).
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OCHEM. J. 126:837-850(1972).
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DLINE: 73008889.
                                               STANDARD;
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Pred. No. 3.54e-16;
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Overy Match 11.0%; Score 16; DB 1: Length 129; Best Local Similarity 100.0%; Pred. No. 2. 64e-21; Matches 16; Conservative 0; Kismatches 0; Indels

Query Match 9,7%; Score 14; DB 1; Length 106; Best Local Similarity 100.0%; Pred. No. 3.54c-15. Matches 0; Indels Matches 14; Conservative 0; Mismatches 0; Indels

EQUENCE: 75059271

M SZILIZE M., RIISCHOMNN N.;

C -1- THE C RECION OF THIS CHINI HAS THE INV (1,2) MARKER.

C -1- THIS IS A BENCE-ONES PROTEIN.

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R HSSP; POLOT; IZM.

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T DOMALN 35 49 FRAMENORK 2.

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T DOMALN 57 89 COMPLEMENTALTY-DETERMINING 1.

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11764 MW; 66DABC95 CRC32; 9.7%;".Score 14: DB 1: Length 108;

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21 RCDIQMTQSPSSLSAS 36

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TITANI K. SHINODA T. PUTNAM F.M.;
BIOL. CHEM. 244:3550-556(1965).
1- THE C REGION OF THIS CIRAIN MAS THE
1- THIS IS A BENCE-JONES PROTEIN.
TH. AOLBEL: RHUNG.
ISSP. PO1607; IREI.

SEQUENCE: 69234734 MEDLINE: 69234734 TITANI K., SHINOI

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12-UUL-1986 (REL. O1. LAST REQUENCE UPDATE)
11-UUL-1986 (REL. O5. LAST ANNOTATION UPDATE)
10 AMPRA CHAIN V-LI RECON (AG).
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Best Local Similarity 100.0%;
Matches 14; Conservative
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SEQUENCE.
HEDLINE: 68362076.
HISCHMANN N.:
HOPPE-SEYLER'S E. PHYSIOL. C
[2]
REVISIONS TO 19 AND 41.
HILGEMANN KO. BARRIEDJ. H.J., HESS M., LANGER B., PONSTINGL R.,
STEINBETT PARTE BARRIEDJ. H.J., WATANARE S.;
L. WATANA
                                                                                                                                                                                                                                                  NYLP 13

NYLP HUMAN STANDARD: PRT: 108 AA.
POLSON: 121-7UL-1966 (REL. 01, CREATED)
21-7UL-1966 (REL. 01, LAST SEQUENCE UPDATE)
01-7AN-1966 (REL. 05, LAST SEQUENCE UPDATE)
101-7AN-1966 (REL. 05, LAST ANNOTATION UPD
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21 DIQMTQSPSSLSAS 34
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DLINE: 76039968.
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USERY 114:6943-6952(1975).
C RECION OF FUTE CHAIN HAS THE INV (1.2) MARKER.
813: A BENCE-COMES PROTEIN.
871: KIHURE.
17: 11-FEB-64.
1801IN U FEB-64.
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CONDENSITABITY - DETERMINING 1
PRAMENORM 2.

CONDERSIMANTY - DETERMINING 2
PRAMENORM 3.

PRAMENORM 4.

BY SHILARITY - DETERMINING 3
PRAMENORM 4.
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Pred. No. 3.54e-16;
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FRAMEWORK 2.
CONFLEMENTARITY - DETERMINING 2.
FRAMEWORK 3.
COMPLEMENTARITY - DETERMINING 3.
FRAMEWORK 4.
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'S MACROGLOBULIN.
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21-UUL 1986 (REL. 01 CREATED)
21-UUL 1986 (REL. 01 LAST SEQUENCE UPDATE)
21-UUL 1986 (REL. 02 LAST SEQUENCE UPDATE)
11-UUL 1986 (REL. 03 LAST SEQUENCE UPDATE)
12-UUL 1986 (REL. 04 LAST SEQUENCE UPDATE)
13-UUL 1986 (REL. 05 LAST SEQUENCE UPDATE)
14-UUL 1986 (REL. 04 LAST SEQUENCE UPDATE)
15-UULARCOTA: METAACA; CHORDATA; VERTEERATA; TETRAPODA; MAM.
21-UULARCOTA: METAACA; CHORDATA; VERTEERATA; TETRAPODA; MAM.
21-UUL 1984 (REL. 04 LAST SEQUENCE UPDATE)

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Query Match 9.7%; Best Local Similarity 100.0%; Matches 14; Conservative

Score 14; DB 1; Len Pred. No. 3.54e-16; 0; Mismatches 0;

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MEDLINE; 76023758. PALM W., HILSCHMANN N.

KYO, MUMAN STANDARD, PRT: 108 AA.
P01607;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-MAR-1992 (REL. 21, LAST ASROTATION UPDATE)
10 AMAR-1992 (REL. 21, LAST ASROTATION UPDATE)
11 AMAR-1992 (REL. 21, LAST ASROTATION UPDATE)
12 AMAR-1992 (REL. 21, LAST ASROTATION UPDATE)
13 AMAR-1992 (REL. 21, LAST ASROTATION UPDATE)
14 AMAR-1992 (REL. 21, LAST ASROTATION UPDATE)
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TAVE, HUMAN STANDARD: PRT: 108 AA.
POLGIO
11.-UL-1986 (REL. 01. CREATED)
21.-UL-1986 (REL. 01. LAST ANDOTATION UPDATE)
01.-UAN-1986 (REL. 05. LAST ANDOTATION UPDATE)
10.-LAN-1986 (REL. 05. LAST ANDOTATION UPDATE)
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RE MEDITIE: PARAGIORE D: U.S.A. 80:4837-4841[1983].

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190352;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
101-NOV-1995 (REL. 32, LAST ANNOTATION UPDAT

SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

KEDLINE: 9908600.

BLANKO D.-B., CHANG C.-H., ALMSNOGTH C., BRUZNGER A.T., EULITE M.,

BOLOMON A., STEYMES F.J., GALIFFER M.;

BLOCHEMISTRY 33.14848-14657(1994).

WESTHOLM F.A., PANAGIOTOPOULOS N., SCHIFFER

RECIGN: BENCE-JONES PROTEIN: 10-ŚTRÔĊTURE.

21 FRAMENOR 1.

34 COMPLEMENTALITI-DETZBAİNING 1.

45 FRAMENOR 2.

46 COMPLEMENTALITI-DETERMINING 2.

70 FRAMENOR 3.

70 FRAMENOR 3.

71 FRAMENOR 4.

Query Match Best Local S Matches 1 h 9.7%; Similarity 100.0%; 14; Conservative Score 14: DB 1: Length 108; Pred. No. 3.54e-16; O: Mismatches O: Indels 41A2388C CRC32;

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STANDARD;

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21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-JNN-1986 (REL. 05, LAST ANNOTATION UPDATE)
10 ANDRA CHAIN V-I RECION (RAU);
100M SAPIEMS (HUMAN) CHORDATA; TETRAPODA; MAMMALIA;
EUTHERITA; PILMATES.

SALITATIONSCORPERSCOSEDIO

SEQUENCE: 71032830

MAZAMARE S., MILSCHMANN N.;

MAZAMARE S., BILSCHMANN N.;

MAPPE-SETLEN'S I. PETSIOL. CHEM. 351:1291-1295(1970).

HER C RECORD OF THIS CHAIN BAS THE INV (3) MARKER.

1- THIS C BENCE-JONES PROTEIN.

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PIR. A01669, MINUMU.

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Query Match 9.7%: Score 14: DB 1; Ler Best Local Similarity 100.0%; Pred. No. 3.54e-16; Matches 14; Conservative 0; Hismatches 0; Length 108; Indels 0

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11671 MW; C8A2EE86 CRC32;

TATILE\_TOTALN STANDARD: PRT: 108 AA.

10139; 1986 (REL. 01, CREATED)
21-701-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-701-1986 (REL. 04, LAST SEQUENCE UPDAT

SEQUENCE. MEDLINE: 72053133. MILSTEIN C.P., DEVERSON

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PRANSHORK 1.

OMPLEMENTARITY-DETERMINING 1.

PRAMSHORK 2.

OMPLEMENTARITY-DETERMINING 2.

PRAMSHORK 3.

PRANSHORK 3.

PRAMSHORK 4.

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BIOCHEM. J. 123:945-958(1971).
-- THE CREGION OF THIS CHAIN HAS THE INV PIR: A01865; KIHUDE. HSSP: P01607; IFVC.

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  Query Match 9.7%;
Best Local Similarity 100.0%;
Matches 14; Conservative
                                       DOMAIN
DISULFID
NON_TER
SEQUENCE
                                       98
23
108
108 AA;
                                     108 B1
108
11810 MW;
Score 14; DB 1; Length 108;
Pred. No. 3.54e-16;
0; Mismatches 0; Indels 0;
                                                        FRAMEWORK 4.
BY SIMILARITY
                                     F5588F47 CRC32;
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TYIE JUNAN STANDARD; PRT; 108 AA.
P01594;
21-701-1986 (REL. 01, CREATED)
21-701-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-JNA-1988 (REL. 05, LAST SEQUENCE UPDATE)
101-JNA-1988 (REL. 05, LAST ANNOTATION UPDATE)
101-JNA-1988 (REL. 06, LAST ANNOTATION UPDATE)
101-JNA-1988 (REL. 07, LAST ANNOTATION UPDATE)
101-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE.
72189444.
MEDLINE: 72189444.
SCHIECHL H., HILSCHMANN N.;
SCHIECHS E., PHYSIOL. CHEM.
FOLORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353:345-370(1972).
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BY YAY CRYSTALOGNAPHT.

BY PELLANASES OF SOLUTIONS M. EPP O., COLMAN P.M., LATTMAN E.E.,

BY PELLANASES OF SOLUTIONS M. EPP O., COLMAN P.M., LATTMAN E.E.,

BY SCHWACER P. STECCHARM M. SCRRAMM H. J.;

BY SCHWACER M. STECCHARM M. STRUCTURE OF THE V REGION OF THE SCHWAL H. STRUCTURE OF THE V REGION OF THE SCHWAL H. STRUCTURE OF THE V REGION OF THE SCHWAL H. STRUCTURE A SECCHARM H. STRUCTURE A SECCHARM M. STRUCTURE A SECCHARM M. SCHWAL M. S 1. TIGH:
1. TIGH:
1. TORSION BENCE-JONES PROTEIN:
1. 23 FRANCHORK 1.
24 GONFLEMENTARITY-DETERMINING 1.
25 GONFLEMENTARITY-DETERMINING 2.
26 GONFLEMENTARITY-DETERMINING 3.
27 GONFLEMENTARITY-DETERMINING 3.
28 FASTINGARITY. 24 50 57 23 23 ç

RESULT 19

RESULT 19

RESULT 19

RESULT 196 (REL. 01, CREATED)

DT 21.JUL.1966 (REL. 01, LAST SEGGENCE UPDATE)

DE 16 KAPPA CHAIN V. V REGION (2606).

CE UPLEALN; RODENTIA.

RESULTS, RODENTIA.

RP SEQUENCE.

RY HELLIN; RODENTIA.

RA JOHNSON N. SLANARD J., PAUL L., HOOD L.;

RA JOHNSON N. SLANARD J., PAUL L., HOOD L.;

RA JOHNSON N. SLANARD J., PAUL L., HOOD L.;

RA JOHNSON N. SLANARD J., PAUL L., HOOD L.;

RA JOHNSON N. SLANARD J., PAUL L., HOOD L.;

RETALORIS, 121:302.307(1982).

CC 1- THIS CHAIN NAS ISOLATED FROM MYELOMA PROTEINS TEAT BI

CC 1- THIS CHAIN NAS ISOLATED FROM HELDMA PROTEINS TEAT BI

CC 1- THIS CHAIN NAS ISOLATED FROM HELDMA PROTEINS TEAT BI

CC 1- THIS CHAIN NAS ISOLATED FROM HELDMA PROTEINS TEAT BI

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THAT BIND

MAMMALIA;

PRAMEMORY 1.
COMPLEMENTARITY DETERMINING 1.
PRAMEMORY 2.
COMPLEMENTARITY DETERMINING 2.
PRAMEMORY 3.
PRAMEMORY 3.
COMPLEMENTARITY DETERMINING 3.

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Ouery Match 9.7%; Score 14: DB 1; Length 108; Best Local Similarity 85.7%; Ped. No. 3.54e-16; Matches 12; Conservative 2; Mismatches 0; Indels

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Caps

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Query Match 9.7%; Best Local Similarity 100.0%; Matches 14; Conservative

Score 14: DB 1: Length 108; Pred. No. 3.54e-16; 0: Mismatches 0: Indels 0;

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NON\_TER 108 SEQUENCE 108 AA;

108 11939 MW; B455AF00 CRC32;

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ESULT 22

D KVZEJMOUSE STANDARD; PRT; 113 AA.

C P03976; REL. 02, CREATED)

T 23-OCT-1986 (REL. 02, LAST SEQUENCE UPDATE)

T 03-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)

T 04-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)

E IG KAPPA CHALIN V-II REGION (17529.1).

E IG KAPPA CHALIN V-II REGION (17529.1).

S HIS MISCULUS (MOUSE).

C ENTRETA, RODENTIA.

MAMMALIA:

TERMINATION OF THE ALTERNATION O

RESULT 21

KV2P\_MOUSE STANDARD: PRT: 113 AA.

10 KV2P\_MOUSE STANDARD: PRT: 113 AA.

11 KV2P\_MOUSE STANDARD: PRT: 113 AA.

12 FOR ALL 1956 (REL. 01. CREATED)

DT 11-UTL-1956 (REL. 27. AST SEQUENCE UPDATE)

DT 12-UTL-1959 (REL. 27. AST SEQUENCE UPDATE)

DT 12-UTL-1959 (REL. 27. AST SEQUENCE UPDATE)

DT 14-UTL-1959 (REL. 27. AST SEQUENCE UPDATE)

DE 16 KAPPA CHARY V.II RECION (7534.1)

OC EUTRATYCT: RETAKON. CHONDATA: VERTEBRATA: TETRAPODA: MAMALIA:

RN 111

RN 111

RN 121

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Query Match Best Local S Matches 1 h 9.7%; Similarity 100.0%; 14; Conservative Score 14; DB 1; Lene Pred. No. 3.54e-16; 0; Mismatches 0; Length 113; Indels 0; Gaps

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RESULT.

1D MACE\_BAT STANDARD; PRT; 106 AA.

AC POISS;

PT 21.-TUL-1996 (REL. 01, CREATED)

PT 21.-TUL-1996 (REL. 01, LAST SEQUENCE UPDATE)

PT 01.-APR-1998 (REL. 07, LAST SEQUENCE UPDATE)

PT 01.-APR-1998 (REL. 07, LAST ANNOTATION UPDATE)

DE 1G MAPR-KUNIN C RESTON, B ALLELE.

OC EUTHERIA, RODENTIA. 100 PYTFGGGTKLEIKR 113 |||||||||||| 115 PYTFGGGTKLEIKR 128

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Query Match Best Local S Matches 1

h 9.7%; Similarity 100.0%; 14: Conservative Score 14: DB 1: Length 113: Pred. No. 3.54e-16: O: Indels Gaps ö

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Gaps

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Best Local Similarity 100.0%;
Matches 13; Conservative
                                                                                                                                                                                         Query Match 9.0%;
Best Local Similarity 100.0%;
Matches 13; Conservative
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WEDLINE: 3021530

WECKEN D.J. BELL M., POTTER M.;

PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).

PROC. NATL. ACAD. SCI. U.S.A. 75:391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STARACE V. QUERINJEAN P.,
J. IMMUNOL. 115:59-62(1975).
PIR: A02117; KIRTD.
HISSP: PO1842: 18AF.
PROSITE: P800290: 16_HEC: 1.
IMMUNOGLOBULIN C REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 26
RV3H_MOGES STANDARD: PRT: 111 AA.
P01660;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
10 GAMPA, CHAIN V-III REGION (PC 3741 AND TEPC 111).
MIS MOSCULUS (MOUSE). MONDATA: VERTEBRATA: TETRAPODA: MANMALIA:
EUTHERIA: RODERITA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE (BENCE-JONES PROTEIN S211).
MEDLINE: 75212238.
STARACE V., QUERINJEAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 PYTFGGGTKLXIKR 108
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115 PYTFGGGTKLZIKR 128
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SHEPPARD H.W., GUTMAN G.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOURNOE FROM N.A.
TRAIN-LOG:
DELINE: 02005897.
HEPPARD N.W., CATMAN G.A.;
RCC. NATL. ACAD. SCI. U.S.A. 78:7064-7068(1981).
                                                                QUENCE (PC 3741).
DILNE: 9073152.
GCERT M. GATMAITAN L., LOR E., SCHILLING
TURE 276:785-790(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DUENCE FROM N.A.
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N > N (IN REF 2)
NISSING (IN REF 2)
E > O (IN REF 2)
E > N (IN REF 2)
S > N (IN REF 2)
S > N (IN REF 2)
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Pred. No. 1.08e-13;
0; Mismatches 0;
                                                                                                                                                                                    Score 13; DB 1; Len
Pred. No. 1.08e-13;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
FRAMEWORK 3.
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;
                                                                                                                                                                                                                     Length 111;
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RESULTS 25

RESULTS 25

ROASSANCESE STANDARD: PRT: 108 AA.

AD ROASSANCESE STANDARD: PRT: 108 AA.

AD ROASSANCESE STANDARD: PRT: 108 AA.

AD ROASSANCE STANDARD: PRATE: 108 AA.

DT 11-AGG_1887 (REL. O5. CEEATED)

DT 11-AGG_1887 (ROSEDATA, VERTEBRATA; TETRAÞODA; MANG

RESULTS 104.350 - 340 (RELETITES G.M., MARKHAM A.F., NILGTEIN G.;

RESULTS 104.350 - 340 (RELETITES G.M., MARKHAM A.F., NILGTEIN G.;

RESULTS 104.350 - 340 (RELETITES G.M., MARKHAM A.F., NILGTEIN G.;

RESULTS 104.350 - 340 (RELETITES G.M., MARKHAM A.F., NILGTEIN G.;

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RESULTS 104.350 - 340 (RELETITES G.M., MARKHAM A.F., NILGTEIN G.;

RESULTS 104.350 - 340 (RELETITES G.M., MARKHAM A.F., NILGTEIN G.;

RESULTS 104.350 
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"TION UPDA.

"ADMAN; VERTEBRATA; TETRA.

JOURNAL D. J., BELL M., POTTER M.;

SEQUENCE (PC 9245).

RATE JOURNAL D. SCI. U.S.A. 75:3913-3917(1978).

SEQUENCE (PC 9245).

RA MEDLIER, 9071557.NM L., LOH E., SCHILLING J., NOOD L.E.;

RA MEDLIER, 9071557.NM L., LOH E., SCHILLING J., NOOD L.E.;

RA MEDLIER, 9071557.NM L., LOH E., SCHILLING J., NOOD L.E.;

RA MEDLIER, 9071557.NM L., LOH E., SCHILLING J., NOOD L.E.;

RA MEDLIER, 907155. NM DE 9241 SEQUENCES ARE IDENTICAL.

PIR, A0195, NM DE 9241 SEQUENCES ARE IDENTICAL.

RESP, POLITY; LOC.

RESP, POLITY; LOC.

100179; LOC.

10179 J. 10179

10189 SS PRAMEMORY

10199 SS PRAMEMORY
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AC PO
DT 23
DT 23
DT 01
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Best Local Similarity 100.0%;
Matches 13; Conservative
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Best Local Similarity
RYJD_MOUSE STANDARD: PRT: 111 AA.
P09377:
23-0CT-1986 (REL. 02, CREATED)
23-0CT-1986 (REL. 02, LAST SEQUENCE UPDATE)
01-0CT-1998 (REL. 27, LAST SEQUENCE UPDATE)
10 FAPPA CHAIN V-III REGION (50610.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGURCE FROM N.A.

REDLINE, 8337/1467.

KAARTIKEN M., GAIFFITHS G.M., MARKHAM A.F., MILSTEIN C.;

KAARTIKEN D4.:20-324(1981).

11. ANTIZ-2 PHEMIT. OXAGOLOME (PROX) ANTIBODY.

REDLI ROOT-45, G-19-6455;

MSSP. D01607; INFALEST.

INGUNOGLOBULIN V REGION. HTBRIDOMA.

INGUNOGLOBULIN V REGION. HTBRIDOMA.

INGUNOGLOBULIN V REGION. HTBRIDOMA.

INGUNOGLOBULIN V REGION.
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SEQUENCE 106 AA; 11732 MW; 35A987EB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYNJ, MODES STANDARD; PRT; 111 AA.
P01662
21-UU-196 (REL. 01, CREATED)
21-UU-196 (REL. 01, LAST REQUENCE UPDATE)
01-CUT-198 (REL. 01, LAST ANDOTATION UPDATE)
10 AUPRA CHAIN VIII REGION (ABPC 22 AND PC 9245).
NUS MISCULUS (MODES) REGION (ABPC 22 AND PC 9245).
RUNAMENTA, RODESTAA, CHORDATA; VERTERNATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODESTAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROC. MAT. ACAD. SCI. U.S.A. 78:7064-7068(1981).
PR. ACALLE KILE.
PROS.TIT. PROJ. 13AP.
PROS.TIT. PROJ. 15 AP.
THOMOMOGRAFILE CREATION.
NON_TER 1.
26 66 INTERCHAIN (WITH A HE DISCULTID 106 106 INTERCHAIN (WITH A HE DISCULTID 106 106 INTERCHAIN (WITH A HE
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115 PYTPGGGTKLEIK 127
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129 ADAAPTVSIFPPS 141
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COMPLEMENTATY DETERMINING 1.
FRANCHORY 2.

COMPLEMENTATY DETERMINING 2.
FRANCHORY 3.

COMPLEMENTATY DETERMINING 3.

COMPLEMENTATY.

BY SANIARATY.
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                                                                                                                                                                                                                                                                                                                                                                                           Score 13; DB 1; Len
Pred. No. 1.08e-13;
0; Mismatches 0;
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RESULT 29

ID NISL, MOUSE STANDARD: PRT; 111 AA.

AC PO166; (REL. 01, CREATED)

DY 21-UL-1966 (REL. 01, CREATED)

PT 21-UL-1966 (REL. 01, LAST SEQUENCE UPDATE)

DY 10-UCT-1993 (REL. 21, LAST SEQUENCE UPDATE)

DY 01-UCT-1993 (REL. 21, LAST SEQUENCE UPDATE)

DY 01-UCT-1993 (REL. 21, LAST SEQUENCE UPDATE)

DY 01-UCT-1993 (REL. 21, LAST SEQUENCE UPDATE)

OC EUTHERIA: RODENTIA.

RE USCALA D.J. BELL H., POTTER H.:

PR SEQUENCE.

RE HELLIE: 79012520.

RE HELLIE: 79012520.

RE HELLIE: 79012520.

RE THIS CHAIR MAS ISOLATED FROM A MYELOMA PROTEIN.

DE TH. 181956. WASCL.

DE HESD: P01279; LGGS.

RM IMMOUSCL.

RM IMMOUSCL.
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STUDENCE.

ACT RODENTIA.

STUDENCE.

ACT TISSUP-EFFERTOMA.

RE HOPPE-SETIEN'S M. PHESIOL. CHEM.

RE HOPPE-SETIEN'S M. PHESIOL. CHEM.

RE PIR. ADDISTA HOPE AND ADDISTANCE.

RE HOPPE-SETIEN'S M. PHESIOL. CHEM.

RE PIR. ADDISTANCE.

RE PIR. ADDISTA
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Best Local Similarity 100.0%;
Matches 13; Conservative
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Best Local Similarity 100.0%;
Matches 13; Conservative
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Best Local Similarity 100.0% Pred. No. 1:08e-13;
Matches 11: Conservative 0; Missatches 0; Indels
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MEDILINE: 79012520.
MEDILINE: 79012520.
MCKKAN D. J., BELL H., POTTER H.;
PROC. NATL ACAD: SCI. U.S.A. 75.39
-1-THIS CHARM WAS ISOLATED FROM A
FIR. A01395; KWRSCI.
HSSD; PO1679; LOGB.
IMMUNOCIOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                  KV39_MOUSE STANDARD; PRT; 112 AA.
P01655 (REL. 01. CREATED)
21.-UU-1996 (REL. 21. AAST SECUENCE UPDATE)
21.-UU-1996 (REL. 27. AAST ANOTATION UPDATE)
22.-UU-1996 (REL. 27. AAST ANOTATION UPDATE)
23.-UU-1996 (REL. 27. AAST ANOTATION UPDATE)
24.-UU-1996 (REL. 27. AAST ANOTATION UPDATE)
25.-UU-1996 (REL. 27. AAST ANOTATION UPDATE)
25.-UU-1996 (REL. 27. AAST ANOTATION UPDATE)
26.-UU-1996 (REL. 27. AAST ANOTATION UPDATE)
27.-UU-1996 (REL. 27. AAST ANOTATION UPDATE)
27.-UU-
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EUNARYOTA: METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA: RODENTIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13; DB 1; Length 112;
Pred. No. 1.08e-13;
0; Mismatches 0; Indels
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CONFLEMENTATY DETERMINING 1.
FRAMEMORY 2.
CONFLEMENTATY DETERMINING 2.
FRAMEMORY 3.
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L. CHEM. 365:1385-1391(1984).
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Pred. No. 1.08e-13;
0; Mismatches 0; indels 0;
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FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3.
FRAMEWORK 3.
BY SIMILARITY.
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                                                                                                                                      Page 45
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TO KATAD MOUSE STANDARD; PRT; 112 AA.

PO1823

PO1823

PO1825

PO18
THE SECTION OF SECTION
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P SECURNOE.

X HEDILINE. 73:433-446(1973).

L J. SECCHEN. 73:433-446(1973).

L J. SECCHEN. 73:433-446(1973).

L J. SECCHEN. 73:433-446(1973).

C I THE C ROCION OF THIS CHAIN HAS THE HWY (3) HAI C C I THE C ROCION. SECCHOLORS PROTEIN.

P SECURNOE. J. LIND.

N IMBORGLOBULIN V ROCION. BENCE-JONES PROTEIN.

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Best Local Similarity 100.0%;
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POLON:

21.-7UL-1986 (REL. OL CREATED)

21.-7UL-1986 (REL. OL LAST SEQUENCE UPDATE)

11.-7UL-1986 (REL. OL LAST SEQUENCE UPDATE)

11.-7UL-1986 (REL. OL LAST SEQUENCE UPDATE)

11.-7UL-1986 (REL. OL LAST SEQUENCE UPDATE)

12.-7UL-1986 (REL. OL LAST SEQUENCE UPDATE)

13.-7UL-1986 (REL. OL LAST SEQUENCE UPDATE)

14.-7UL-1986 (REL. OL LAST SEQUENCE UPDATE)

15.-7UL-1986 (REL. OL LAST SEQUENCE UPDATE)

16.-7UL-1986 (REL. OL LAST SEQUENCE UPDATE)

17.-7UL-1986 (REL. OL LAST SEQUENCE UPDATE)

17.-7UL-1986 (REL. OL LAST SEQUENCE UPDATE)

18.-7UL-1986 (REL. OL LAST SEQUENCE UPDATE)

19.-7UL-1986 (REL. OL LAST SEQUENCE UPDATE)
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                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDILINE 32059477.
HAMININ P.H., GAIT M.J., MILSTEIN C.;
MUCLEIC ACIDS RES. 9:4485-4494(1981).
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01.-JAN-1986 (REL. 05, LAST ANNOTATION UPDATE)
1G KAPPA CHAIM V-I REGION (NI).
1G KAPPA CHAIM V-I REGION (NI).
1GHONG SADIENS (HUMAN).
1GUARGOTA, METAROA, CHORDATA; VERTEBRATA; TETRAPODA; KNAMALIA;
1GTHERIA; PRIMATES.
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115 PYTFGGGTKLEIK 127
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Pred. No. 1.08e-13;
0; Mismatches 0;
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Pred. No. 1.08e-13;
0; Mismatches 0; Indels
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RESULT 194AN STANDARD: FACE POLSTS: DT 21-JUL-1986 (REL. 01, CREATED)

PRT;

112 ζ

SEQUENCE OF 30-136.

MEDLINE; 73053310.

SVASTI J. MILSTEIN C.;

BYOCHEM, J. 128-427-444(1972).

EMBL; Y00810; G52140; ALT\_TERM.

PIR; A01917; KVMS21.

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JOB (RL.
JOBA) (RELLY L.
REPLETA, ROBENTA, CHORDA.

RIPHERIA, ROBENTA, SOLOTE,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sandon service in the service of the
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SEQUENCE: 91054757.

RX MEDILINE: 91054757.

RX MEDILINE: 91054757.

RL PROC. INTIL. ACAD. SCI. U.S.A. 777.4770-4774(19980).

CC -1- THIS CHAIN MS. ISOLATED FROM A WILDOMA PROTEIN TRAT BIND GALACTAN.

RE RITE: A01941; KNSAM.

RE HISS: POLTS: ACAD.

RE HISS: POLTS: ACAD
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RESULT NO AC EU CA RAC SEE ST
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Best Local Similarity 100.0%;
Matches 13; Conservative
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                                                                            TYNN MOUSE STANDARD: 9 PRT: 108 AA.

POLGAT:

21-TUL-1966 (REL. 01. CREATED)

21-TUL-1966 (REL. 01. CREATED)

21-TUL-1966 (REL. 01. LAST ANNOTATION UPDATE)

10 NOFTA (RAIN V-V REGIO (RP 1242).

10 ANDFA (RAIN V-V REGIO (RP 1242).

EURAMPOTA: METALOA; CHORDATA; VERTEBNATA: TETRAPODA;

EUTHERIA: RODENTIA.
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PO1641; 1986 (REL. 0). CREATED;
21. JUL-1986 (REL. 0). CREATED;
21. JUL-1986 (REL. 0). ASS. SECURIOR UPDATE;
21. JUL-1980 (REL. 0). ASS. SECURIOR UPDATE;
21. JUL-1980 (REL. 0). ASS. SECURIOR (MOPO. 173).

10. MARCHA CHAIN (MOPO. 173).

10. MARCHA CHAIN (MORDATA: VERTEBRATA: TETRAPODA: DUTHERATA: ROTERAPODA: DUTHERATA: ROTERAPODA: DUTHERATA: ROTERAPODA: DUTHERATA: ROTERAPODA:
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POLOTE:
1-UUL-1086 (REL. 01 ACREATED)
21-UUL-1086 (REL. 01 ACREATED)
10-UUL-1086 (REL. 01 
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117 TFGGGTKLEIKR 128
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SEQUENCE 107 AA; 11554 MW; 609EDE13 CRC32;

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EVALADOSE STANDARD; PRT; 107 AA.

C PO1675;

T 21-7UL-1986 (REL. 01. CREATED)

T 21-7UL-1986 (REL. 01. LAST SECURNCE UPDATE)

T 01-0CT-1993 (REL. 27. LAST ANGURACE UPDATE)

T GLADPA CHAIN U-VE SECURN (XERC 44).

S MUS MUSCULUS (MODIS) AGOSTON (XERTESRATA: TETRAPODA; MAN UPLITARIA; RODENTIA.
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Best Local Similarity 100.0%;
Matches 12; Conservative
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Best Local Similarity 100.0%;
Matches 12; Conservative
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MEDLINE: 7002830.

RAO D. N. TRUTKOFF S., POTTER H.:

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117 TFGGGTKLEIKR 128
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PA.545.2 (REL. 01. CREATED)
21.-JUL-1986 (REL. 01. CREATED)
21.-JUL-1986 (REL. 01. CAST SECORENCE UPDATE)
21.-JUL-1986 (REL. 01. LAST ANDOTATION UPDATE)
10. CAPPA (CRAIN V-V REATON (RP 9107).

RUNANFOTA, METATACOA; CHONDATA; VERTEBRATA; TETRAPODA; MANNALIA;
EUTHERYCTA, METATACOA; CHONDATA; VERTEBRATA; TETRAPODA; MANNALIA;
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117 TPGGGTKLEIKR 128
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88 BY SIMILARITY.

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11965 MW; 84754175 CRC32;
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Pred. No. 2.85e-11;
0; Mismatches 0; Indels
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## SIDEMENCE.
## SECONDECT.
## STAIN-N.2159934.

RX HEDLINE: ## STAIN-N.2159934.

RX HEDLINE: ## STAIN-N.2159934.

RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).

CC -1- ANTI-RESORATE HYBRIDONA PROFEIN.

DR PIR. A01971: WYSMAN.

RESSP: PO1607; IPAI.

PROMAIN 1 1 23 PANATONNE ANTIBODY.

PROMAIN 1 1 24 COMPLEMENTAINT-DETERNET DOMAIN 57 88 COMPLEMENTAINT-DETERNET DOMAIN 98 108 PANATONNE NATURE DOMAIN 98 11910 MFS 64462905 CRC31:

**GROUP TO THE PROPERTY OF THE PANATONNE NATURE NATURE DOMAIN 98 11910 MFS 64462905 CRC31:

**GROUP TO THE PANATONNE NATURE                                                                                                                                                                          RESULT JO

LOUNTS, AUGUSE STANDARD: PRT: 108 AA.
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                                                      Query Match 8.3%;
Best Local Similarity 100.0%;
Matches 12; Conservative
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Best Local Similarity 100.0%;
Matches 12; Conservative
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117 TFGGGTKLEIKR 128
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                                            Score 12; DB 1; Length 108;
Pred. No. 2.85e-11;
0; Mismatches 0; Indels
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Pred. No. 2.85e-11;
0; Mismatches 0; Indels
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
BY SIMILARITY.
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ANOTHER PROPAGE

ANOTHER PROPAGE

CC 1- THE SECOND AND THE DEPTICAL HAPPER D.G.;
WHICH IT SHARES CERTALH HOTOTYPIC DETENHANTS.

CC 1- THIS CHAIN MAS ISOLATED FROM AN IGN WITH ANTI-GARMA GLOBULIN

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ID KV5P_MOUSE
AC P01649;
                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 1
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Similarity 100.0%;
12; Conservative
                        STANDARD;
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Pred. No. 2.85e-11;
0; Mismatches 0; Indels
                        PRT;
                   108
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P SEQUENCE.

RC STRAIN-A/17

RC STRAIN-A/17

RC CAPA J.D., TING A. 5., NISONOFF A.:

RL ALFELE: 77250895.

RL CAPA J.D., TING A. 5., NISONOFF A.:

RE ALO SIGNATURE POLICONING SUBSTITUTIONS

CC LIGHT CHAIMS. PERFORMAN NING THE POLICONING SUBSTITUTIONS

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CC LIGHT CHAIMS. PERFORMAN NING SUBSTITUTIONS

RESERVED NING SUBSTITUTIONS

RE
                                                                                                                                                                            TO KVSH_MOURE STANDARD: PRT: 108 AA.

C 001646:
DT 21.-UU-.1986 (REL. 01, CREATED)
DT 21.-UU-.1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01.-CUT.-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT 01.-CUT.-1993 (REL. 27, LAST SEQUENCE UPDATE)
DE 1G KAPPA CHAIN V-V RECION (HP 12386).
OS HUS MUSCULUS (MOURS)
OS UPDATION RODENTA. CHORDATM; VERTEBRATM; TETRAPODA; MAMMALIA;
CC SUTHRAIN; RODENTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.-UL-1996 (REL. 01, CREATED)
21.-UL-1996 (REL. 01, LAST ARROCATION DEDATE)
01.-OT-1993 (REL. 07, LAST ARROCATION DEDATE)
1G ALPPA CRAIN V-V REGIONS (ANTI-ARSONATE ANTIBODIES).
RUSARFOCTA, RETARDA, CHORDATA; VERTEBRATA; TETRAPODA; MANMALIA;
EULARFOTA, METARDA, CHORDATA; VERTEBRATA; TETRAPODA; MANMALIA;
7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17. ISA.
LIN V REZION; ANTIANSONITE ANTIBODY.
24 34 CPALEMORY AITY-DETE
35 49 PALEBORY AITY-DETE
57 56 COMPLEXENTALITY-DETE
57 56 COMPLEXENTALITY-DETE
57 80 97 COMPLEXENTALITY-DETE
69 97 COMPLEXENTALITY-DETE
73 80 PERMEDOR 31
108 AM: 12056 MM; 371ED033 CRC32;
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FRANCHORE 2.
COMPLEMENTARITY - DETERMINING 2.
FRANCHORE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 12: DB 1: Length 108;
Pred. No. 2.85e-11;
0: Mismatches 0: Indeis
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                                                                                                                        W 14.

(P SEQUENCE.

AC STRAINAN/J;

AC STRAINAN/J;

RX HEDLINE;

RA SIZEZEMAN M. CADA, J.D.;

RA SIZEZEMAN M. CADA, ST. U.S.A. 78:7679-7683(1981).

CC 1- ANTI-ARSONATE HEBRIDONA PROTEIN.

CC 1- ANTI-ARSONATE HEBRIDONA PROTEIN.

DR HESP: PO1607; LPAI.

EMPUNGALOBULIN V RESION; ANTIARSONATE ANTIBODY.

KW IMPUNGALOBULIN V RESION; ANTIARSONATE ANTIBODY.

KW IMPUNGALOBULIN V RESION; ANTIARSONATE ANTIBODY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mon
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STRAIN-A/J.

X REDLINE, 0215094.

X RESP. POISO? INFA.

R RIR. A0157; KYMSAR.

R RIR. A0157; KYMSAR.

R RIR. A01518 V REZION: ANTIARSONATE ANTIBODY.

R RIR. A01518 V REZION: ANTIARSONATE ANTIBODY.

R RESP. POISO? INFA.

R RESP. POISO? INFA.

R RANDROGE 1.08 ANTIARSONATE ANTIBODY.

R RANDROGE 1.08 ANTIARSONATE ANTIBODY.

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PO DOMAIN 57 88 PAREMONENT.

PO DOMAIN 58 PARE
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Best Local Similarity 100.0%;
Matches 12; Conservative
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PRAMENOR 1.

COMPLEGENTARIT - DETERMINING 1.

PRAMENOR 1.

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Pred. No. 2.85e-11;
0; Mismatches 0;
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Query Match 8.3%; Best Local Similarity 100.0%; Matches 12: Conservative

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Best Local Similarity 100.0%; Pred. No. 2.85e-11; Matches 12; Conservative 0; Mismatches 0; Indels

3 QMTQSPSSLSAS 14 ||||||||||||| 23 QMTQSPSSLSAS 34

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SEQUENCE 24 35 50 57 57 89 98 98 23 108 **NA**; COMPLEMENTATIV-DETERMINING 1.
FRAMENCHE 2.
COMPLEMENTATIV-DETERMINING 2.
FRAMENCHE 3.
FRAMENCHE 4.
FRAMENCHE 4.
EY SIMILARITY.

Query Match 8.3%; Best Local Similarity 100.0%; Matches 12; Conservative Score 12: DB 1: Length 108: Pred. No. 2.85e-11; 0: Mismatches 0; Indels 0;

11961 MW;

58067780 CRC32;

97 TFGGGTKLEIKR 108 |||||||||||| 117 TFGGGTKLEIKR 128

NYT\_HUNAN STANDARD: PRT: 109 AA.

101612.
21-UU-1086 (REL. 01, CREATED)
21-UU-1086 (REL. 01, LAST ANNOTATION UPDATE)
10-ANN-1088 (REL. 06, LAST ANNOTATION UPDATE)
10 ANNA UPDATE;
11 ANNA UPDATE;
11 ANNA UPDATE;
12 ANNA UPDATE;
12 ANNA UPDATE;
13 ANNA UPDATE;
14 ANNA UPDATE;
15 ANNA UPDATE;
16 ANNA UPDATE;
16 ANNA UPDATE;
17 ANNA UPDATE;
18 ANNA UPDATE;
18 ANNA UPDATE;
19 ANNA UPDATE;
10 ANNA UPDATE;
11 ANNA UPDATE;
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12 ANNA UPDATE;
13 ANNA UPDATE;
14 ANNA UPDATE;
16 ANNA UPDATE;
16 ANNA UPDATE;
17 ANNA UPDATE;
18 ANNA UPD

Query

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SEQUENCE OF 30-149.

SEQUENCE OF 30-149.

SEATTH G. P. 18486617.

SEATTH G. P. 171.337-347(1978)

BIOCHEM. J. 171.337-347(1978)

THE MATCHER CHAIN HAS 13 ADDITIONAL RESIDURES AT ITS CONTROL OF 36 NOCLEOTIDES AT ITS CONTROL OF 36 NO
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MEDILHE: BO176554.
RABBITTS T.H., BAMIN P.H., MATHYSSENS G., ROE B.A.;
RABBITTS T.H. S8:176-187(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-71 FROM N.A.

MEDLINE; 83001944.

KELLEY D.E., COLECLOUGH C., PERRY R.P.;

CELL 29:681-689(1982).
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S AFTER THE CODON
E AMINO-TERMINAL
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PRODUMENT STORE OF THE STORE OF
          8.3%;
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COMPLEMENTA TUTY - DETERMINING 1.
FRAMEWORK 2.
COMPLEMENTA TUTY - DETERMINING 2.
FRAMEWORK 3.
COMPLEMENTA TUTY - DETERMINING 3.
FRAMEWORK 4.
BY SHILARTY - DETERMINING 3.
Score 12; DB 1;
          Length
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SEQUENCE:

STRAIN-N/2:

STRAIN-N/2:

STRAIN-N/2:

STRAIN-N/2:

STRAIN-N/2:

STRAIN-N/2:

STRAIN-N/2:

A MONOTHY 3: MARGOLIZES M.N.;

A BICCHMISSERIA 2:1.13:2.118 (1983);

A BICCHMISSERIA 2:1.13:2.118 (1983);

LE CHARLES COLUMNA:

DE PIR. AD19:1. CAMBES

MESSP. POLGOT: 1001

PRANTONE I.

PRANTONE III I.

PRANTONE III.

PRANTONE I.

PRANTONE III.

PR
                                                                                         Db 102 TFGGGTKLEIKR 113
|||||||||||
gy 117 TFGGGTKLEIKR 128
RESULT 46
ID KV5A_MOUSE
                                                                                                                                                                                     Query Match 8.3%;
Best Local Similarity 100.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                24
40
55
62
94
103
113
113
113
   STANDARD;
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FRANCHORE 2.
COMPLEMENTATIT - DETERMINING 2.
FRANCHORE 3.
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FRANCHORE 4.
FRANCHORE 4.
                                                                                                                                                                                         Score 12; DB 1; Length 113;
Pred. No. 2.85e-11;
0; Mismatches 0; Indels
   PRT;
149
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TO EAPPA CHAIN V-N REGION (MPCII)
PRANEHONER, 1
COMPLEMENTARITY DETERMINING 1.
PRANEHORE 2.
COMPLEMENTARITY DETERMINING 2.
PRANEHORE 2.
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PRANEHORE 3. RESULT PACE POINTS AC POINTS POINTS POINTS POINTS POINTS POINTS POINTS RESULT RA HEDDEN RA HEDDE Query Match 7.6%; Best Local Similarity 100.0%; Matches 11; Conservative 117 TFGGGTKLEIKR ₹ STANDARD; 128 11876 MW; Score 11; DB 1; Len Pred. No. 6.36e-09; 0; Mismatches 0; 3B5013E3 CRC32;

US-08-836-455-2.rsp

SECURNE. 79.95288.
MEDLINE. 79.95288.
J. THOUNDE. 121.1905-1910(1979).
J. THOUNDEL 121.1905-1910(1979).
HORING AND HOLD FROM HYELOMA PROTEINS THAT BIND BETA(2-1)-FROCTOPURANOSTL MOIETIES (INULIN).
PIR: 892808. KYMSO9.
HSSP. PO1807. LYD. PONSŠI. 1986 (REL. 01, CREATED)
21.-UI.-1986 (REL. 01, CREATED)
01.-UI.-1996 (REL. 01, LAST SEQUENCE UPDATE)
01.-UI.-1991 (REL. 27, LAST SEQUENCE UPDATE)
101 CAMPA, CHALTH V-V RECION (EPC 109).
101 MADOLINS, CHOUSE),
101 MANUAL, MODERIA,
101 MANUAL,
101 MANUAL,
102 MANUAL,
103 MANUAL,
103 MANUAL,
104 MANUAL,
105 MANUAL,
105 MANUAL,
107 MANUAL,
108 MANUAL,
108 MANUAL,
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108 MANUAL,
108 MANUAL,
109 MANUAL, PRAMEMORY 1.
COMPLEMENTATIV-DETERMINING 1.
PRAMEMORY 2.
COMPLEMENTATIV-DETERMINING 2.
PRAMEMORY 3.
PRAMEMORY 4.
PRAMEMORY 4.
FRAMEMORY 4.
ET STATIARTY DETERMINING 3. 108 AA

RESULT
AC PO
AC PO
DT 21
DT 21
DT 21
DT 11
OS MT LT 48

RYJA\_MOUSE STANDARD; PRT; 111 AA.

PO155; 196 (REL. 01, CREATED)
21.-UU-1986 (REL. 01, LAST SEQUENCE UPDATE)
21.-UU-1986 (REL. 27, LAST SEQUENCE UPDATE)
01.-CCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
10.-CCT-1993 (REL. 27, LAST ANNOTATION UPDATE)

Length 108 Indels 0

Gaps 0

Query Match 8.3%; Best Local Similarity 100.0%; Matches 12; Conservative

Score 12; DB 1; Ler Pred. No. 2.85e-11; O; Mismatches O;

Length 149; ll; 0; Indels

0:

Gaps 0 Š

16434 MW

F225F977 CRC32;

138 TFGGGTKLEIKR 149

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US-08-836-455-2.rsp

EUKĀRYOTĀ; METĀSOĀ; CHORDĀTĀ; VERTEBRATĀ; TETRAPODĀ; MAMMĀLIĀ; EUTHERIĀ; RODENTIĀ.

H [1]

D SEQUENCE. 79073152.

X MEDICARE. 79073152.

RI MUTURE 776:78073781.

RI MUTURE 776:7807 FRAMENORK 1.
CONFLICTION THY - DETERMINING 1.
FRAMENORK 2.
CONFLICTION TO - DETERMINING 2.
FRAMENORK 3.
FRAMENORK 3.
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Ouery Match 07 64; Score 11; DB 11, Length 111; Best Local Similarity 100 04; Pred, No. 616c-09; Stocob; Matches 11; Conservative 0; Hismatches 0; Indels 0;

å å 101 TFGGGTKLEIK 111 ||||||||| 117 TFGGGTKLEIK 127

TYCL 49

TYCL\_MOUSE STANDARD: PRT: 111 AA.

PO1656;
21-UL-1986 (REL. 01, CREATED)
21-UL-1986 (REL. 01, LAST ESOCRENCE UPDATE)
01-CT-1993 (REL. 27, LAST ESOCRENCE UPDATE)
1C KAPPA CHAIN V-III REGION (MOPC 70).

MUS MUSCULS (MOUSE).
MUS MUSCULS (MOUSE).
1CHIRENTA: NOTESTANO, CHORDATA: VERTEBRAIA: TETRAPODA: MAMOALIA;
1CHIRENTA: NOTESTANO.

SEQUENCE.

HEDLINE: 67056897.

GRAY W. F., DERTER W. J., HOOD L.E.;

SCIENCE 155.465-467(1967).

--- THIS IS A BENCE-JONES PROTEIN.

PIR: A01990; KV8580.

HSSP. PO1179; IGGB.

8

Mon

Apr 19 13:23:53 1999

Search completed: Thu Apr 15 18:03:29 1999 Job time: 52 secs.

US-08-836-455-2.rsp

V REGION; BENCE-JONES PROTEIN.

1 23 FRAMEWORK 1.

Page 63

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Mon Apr 19 13:23:53 1999
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Page 61

US-08-836-455-2.rsp

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Query Match 27 (8); Score 11; DB 1; Length 111; Best Local Similarity 100 09; Pred No. 6 (36-09; Indels 0; Matches 11; Conservative 0; Hismatches 0; Indels 0; Gaps

101 TFGGGTKLEIK 111 ||||||||| 117 TFGGGTKLEIK 127

RESULT 50

RESULT 50

RYST\_MOUSE STANDARD: PRT: 111 AA.

ID RYST\_MOUSE STANDARD: PRT: 111 AA.

ID RYST\_MOUSE (REL. 01, CREATED)

2 1-3TL-1386 (REL. 21, LAST REZOUENCE UPDATE)

DT 21-3TL-1386 (REL. 21, LAST REZOUENCE UPDATE)

DT 10-3TL-1386 (REL. 21, LAST REZOUENCE UPDATE)

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\*\*PT DOMAIN J. 33 CORPLEMENTARITY - DETERMINING 2.

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\*\*PT DOMAIN J. 35 FAMEDORK 3.

\*\*PT DOMAIN J. 36 FAMEDORK 3.

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Ouery Match 7.6%; Score 11. DB 1; Length 111; Best Local Similarity 100 0%; Pred. No. 6. 36e-09; Matches 11; Conservative 0; Mismatches 0; Indels 0 Gaps

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Database Release Information:

2. database SWISS-PROT, Release 36.0, Released on 18Jul1998, Formatted on 18Aug1998

Combined SPIREMBL, Release 8.0, Released on 21Nov1998, Formatted on 15Dec1998

Word-size: 5 Words: 77835 Diagonals: 14,908 Total-diagonals: 118,698,092

Integral-width: 1 Alphabet: 20 List-size: 50 CPU minutes: 9.51
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SW: KV5M_MOUSE
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Match

Description

## Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U Distribution rights by Oxford Molecular Ltd onit.

Rup MPsrch\_pp 9 protein - protein database search, using Smith-Waterman algorithm Thu Apr 15 18:03:46 1999; MasPar time 10.56 Seconds 683.516 Million cell updates/sec

Tabular output

Title: Description: Perfect Score: Sequence: >US-08-836-455-2 (1-145) from USO8836455.pep 145 1 MGAPAQTIGFILLLEPFGTRC......

. IXRADAAPTVSIFPPSSKLG

Scoring table: TABLE unitprotable Gap 60

Post-processing Searched: Minimum Match 0% Listing first 1000 summaries 165420 seqs, 49795644 residues

optramble

1 sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human

5:sp\_invertebrate issp\_mammal 7:sp\_mhc 8:sp\_organtlia

9:sp\_bhage 10:sp\_bant 11:sp\_rodent 12:sp\_unclassified

13:sp\_vertebrate 14:sp\_virus

Pred. No. is the number of results predicted by chance to have a sorre of the result being printed, and is determined the result being printed, and is derived by analysis of the total score distribution. Mean 3.371; Variance 0.503; scale 6.702

SUMMARIES

Result Query

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U8-08-836-455-2.rept

Page 3

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RESULT 1
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AC 01538 PRELIMINARY: PRT: 117 AA.
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DT 01-AG: 1998 (TREDBLEEL 0): AAST ANGALTON UPDATE)
DE 104UDOGLOBULIN WARIABLE REGION, KAPPA LIGHT CHAIN (FRAGMENT).
GS VYLA.
OS HONO SAPIENS (HUNAN).
CC EUVAROTA: PRIMATES.
CC UTHERIA: PRIMATES.
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STRAIN-CHIMEN-LPRILDR:
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GILKESON G.S.,
SUBMITTED (MN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: US9155; G1389781:
EMBL: US9155; G1389781:
EMBL: US9155; G1389781:
EMBL: US9155; G1389781:
EMBL: US9155; G1
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01-NOV-1996 (TREMELEEL OL LAST SOURCE UPDATE)
01-NOV-1996 (TREMELEEL OT, LAST ANNOTATION UPDATE)
ANTI-DUA LIGHT CHAIM (FRAGERY).
WIS MUSCULUS (MOUSE).
MUS MUSCULUS (MOUSE).
RUINAROTA. METACOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMALIA:
UTHERIA: NOVERTIA.
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DAN REARRANCED BY A 7(12) TRANSLOCATION LEADING TO BURKITT'S LYRCHONA
IN THE CELL LINE 31 (CLONE 31P).
HONO SAPIENS (HOMAN).
EUGHARYOAL METAKOAL CHORDATA: VENTEBRATA; TETRAPODA; MANNALIA;
EUGHARYOAL METAKOAL CHORDATA: VENTEBRATA; TETRAPODA; MANNALIA;
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MEDILHE: 87259867.

KLOBECK H.G., COMBRIATO G., EACHAU H.G.,

MICHEIC ACIDS RES. 15:4877-4888(1987).

EMBL, X05929; E12675;

SEQUENCE 50 AA; 5486 MM; 65586619 CRC
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BMITTED (AUG-1987) TO EMBL/GENBANK/DDBJ
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108 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16: DB 4; Length 50;
Pred. No. 1.21e-18;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65586C19 CRC32;
                                                                            2084FEDC CRC32;
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LCHAR PROTEIN
LCHAR PROTEIN
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90X-PROTEASE (BACILLOP
NUCLEAR RECEPTOR COACT
N-METHYL-D-ASPARTATE R
COSNID 771.
RB18A PROTEIN.
RB18A PROTEIN PR
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PUTNITUE ACIT-ON EVET
CHITIN ENTRASE.
REDEDAGEN (PROFILAGRI
UNCONVENTIONAL MYGGIN.
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DACHSHUND VARIANT 1.
P-TYPE ATPASE 2.
LATS.
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DO 035971 PRELIMINARY PRT: 114 AA.
AC 035971 PREMILEL. 05. CREATED)
DT 01-JAN-1988 (TREMBLEL. 05. LAST SECORECE UPDATE)
DT 01-JAN-1988 (TREMBLEL. 05. LAST SECORECE UPDATE)
DT 01-JAN-1988 (TREMBLEL. 05. LAST SECORECE UPDATE)
DE ANTI-ACID PHOSPHATASE VARIABLE LIGHT CHAIN 11 (PRAGMENT).
OR EUTKARYONA, METAZOA. CRORDATA: VERTERRATA, TETRAPODA: MAMMALIA:
OR EUTKARYONA, METAZOA. CRORDATA: VERTERRATA, TETRAPODA: MAMMALIA:
OR EUTKARYONA, METAZOA. CRORDATA: VERTERRATA, TETRAPODA: MAMMALIA:
OR EUTKARYONA, METAZOA.
OR EUTKARYONA, 
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ID 035842; PRELIMINARY; PRT; 262 AA.

AC 035843; PREMILERI. 05, CREATED)

DT 01-JAN-1998 (TREMILERI. 05, LAST SECURACE UPDATE)

DT 01-JAN-1998 (TREMILERI. 05, LAST SECURATION UPDATE)

DT 01-MOS-1998 (TREMILERI. 05, LAST SECURATION UPDATE)

DE ANTI-HIV-1 REVERSE TRANSCRIPTASE SINGLE-CHAIN VARIABLE FRAGMENT.

ON EUTHARTONA, METALOA, CHORDATA, VERTEBRATA; TETRAPODA; MAMMALIA;

RN 11

RN 2502ECCE FROM M. A.

RN 2502ECCE FROM M. A.

RN 2502ECCE FROM M. A.

SHAREEN F., DUNN L., 28U M., BAGASRA O., POMERANTZ R.J.;

RR 2502ECCE GROWN CARDOLLASSO.)

RR 2502ECCE DUNN CARDOLLASSO.)

RR 2502ECCE DUNN L., 27842 MM; ANFALDERS CRC32;

DR 2502ENERCE 262 AA. 27842 MM; AP24DBF6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mon
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ID Q15533
AC Q15533;
DT 01-NOV-1996
DT 01-NOV-1996
RESULT
10 099822 PRELIMINARY, PRT; 112 AA.
10 999822 PRELIMINARY, PRT; 112 AA.
11 099822 PRELIMINARY, PRT; 112 AA.
12 099822 PREDIMEREL 03, CREATED)
10 10 -4MX-1997 (PREDIMEREL 05, LAST RESOURCE UPDATE)
11 01 -4MY-1997 (PREDIMEREL 05, LAST REMOVATION UPDATE)
12 01 -4MY-1997 (PREDIMEREL 05, LAST REMOVATION UPDATE)
13 01 -4MY-1997 (PREDIMEREL 05, LAST REMOVATION UPDATE)
14 01 -4MY-1997 (PREDIMEREL 05, LAST REMOVATION UPDATE)
15 01 -4MY-1997 (PREDIMEREL 05, LAST REMOVATION UPDATE)
16 01 -4MY-1997 (PREDIMEREL 05, LAST REMOVATION UPDATE)
17 01 -4MY-1997 (PREDIMEREL 05, LAST REMOVATION UPDATE)
18 01 -4MY-1997 (PREDIMEREL 05, LAST REMOVATION UPDATE)
19 01 -4MY-1997 (PREDIMEREL 05, LAST REMOVATION UPD
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Best Local S
Matches 1
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 9.0%; Score 13; DB 11; Le Best Local Similarity 100.0%; Pred. No. 7.81e-12; Matches 13; Conservative .0; Mismatches 0;
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TISSUE-KTREITOMA:
MEDILIE: 96211469
SHAREN F. DORNA L. BHU M., BAGASRA O., POMERANTZ
SHAREN F. DORNA L. 2010 (1996)
EMB. U48716-2199026:
PRIM. 1970047; 19.
RNA-DIRECTED DIA POLYMERASE.
SEGUENCE 262 AA; 27842 NW; AF24DBF6 CRC32;
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SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL. T14655; E1169595; -
FRAM: PP00047; 19
NON_TER 117
SEQUENCE 117 AA; 12748 MM; 034081EP CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                102 TFGGGTKLEIKRA 114
|||||||||||
117 TFGGGTKLEIKRA 129
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Similarity 100.0%; Pred. No. 8.82e-26;
19; Conservative 0; Mismatches 0;
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LAST SEQUENCE UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 114;
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SEQUENCE FROM N.A.
TISSUE-FORE-MARGH,
DITTEL, JANABON,
DITTEL, JANABON,
BARBAC C.F., DERTON D.R.; I., BINLEY J.M., SODROSKI J., MOORE J.P.,
BARBAC C.F., DERTON D.R.;
EURNITTED (DEC-1955) TO EMBL/GENBANK/DDBJ DATA BANKS.
DRL; UB2768, 10125570;
DRJ; UB2768, 10125570;
BPAM; PD00047; 149.
NON TEB 1112 AA; 11905 NM; 40E0259D CRC12;

Query Match 83%; Score 12; DB 4; Length 112; Best Local Similarity 100.0%; Pred. No. 1.16e-09; Indels Matches 12; Conservative 0; Mismatches 0; Indels 0

Gapa

98 TFGGGTKLEIKR 109 ||||||||||| |117 TFGGGTKLEIKR 128

C4.121.

PRELIMINARY: PRT: 127 AA.

06.123.
01.40V-1996 (PREMEREI, 01. CREATED)
01.40V-1996 (PREMEREI, 02. LAST RAUDINGE UPDATE)
01.40V-1996 (PREMEREI, 05. LAST RAUDINGE UPDATE)
01.40V-1998 (PREMEREI, 05. LAST RAUDINGE UPDATE)
ANTICEN, B-CELLE RECEPTOR PRECURSOR.

REGIONAL RECEPTOR PRECURSOR.

EURANOSA, CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EURANGELA; RODENTA.

\$ B

229 TFGGGTKLEIKR 240 |||||||||||| 117 TFGGGTKLEIKR 128

P97771 PRELIMINARY, PRT. 241 AA.

P97771 PRELIMINARY, PRT. 241 AA.

197771 PRESIDENCE. 03. CREATED

01-MA'-1997 (TRESGLENCE. 03. LAST SEQUENCE UPDATE)

10-TON-1999 (TRESGLENCE. 05. LAST SEQUENCE UPDATE)

10-TON-1999 (TRESGLENCE. 05. LAST SENOTATION UPDATE)

10-TON-1990 (TRESGLENCE. 05. LAST SENOTATION UPDATE)

10-TON-1990 (MOUSE)

10-TON-1990

SECUENCE FROM N.A. YI K.S., SUH P.G., RYU S.H., CHOI S.J., KIM H.J., KIM H.J., CHOI S.H., CHOME H.K.;
KIM H.J., CHOI H.H., CHUMG H.K.;
SUBHITTED (FEB-1997) TO BEBL/GENBANK/DDBJ DATA BANKS.
BIBLI, UBBO67; G180546; D.B.
FFAM: PFO0047; 1.9.

241 AA;

241 1: 26086 MW;

EBB2D29D CRC32;

Query Match 8.3%; Score 12; DB 4; Len Best Local Similarity 100.0%; Pred. No. 1.16e-09; Matches 12; Conservative 0; Mismatches 0;

Length 240;

0

NON\_TER 1 1 NON\_TER 240 240 SEQUENCE 240 AA; 25569 NW; 6472A9C9 CRC32;

SEQUENCE FROM N.A., WING M.G., WINTER G.; NAT. BIOTECHNOL. 15:629-631(1997). ENGL: Y1056: E315281; -. PPAM: FF00047; ig. NON\_TER 1 1

QUENCE FROM N.A. RAIN-BALB/C;

MEDILHE: 96144009 THIRIDUS S. MOTMANS K. HETLIGEN H., RAUS J., LUCUNOCENTICS 43.167-168(1996). EMBL: 435681 6699073: \*\*. EMAN, POCCO47: 19.

Query Match 8.3%; Score 12: DB 11: Length 127; Best Local Similarity 100.0%; Pred. No. 1.16s-09; Natches 12: Conservative 0; Missatches 0; Indels 0; SIGNAL 1 19 POTENTIAL.
CHAIN 20 127 ANTICEN, B-CELL RECEPTOR.
SEQUENCE 127 AA; 13656 NW; C096D809 CRC32;

115 TFGGGTKLEIKR 126 |||||||||| 117 TFGGGTKLEIKR 128

ğ ş

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0 Length 244;

TRESULT 11

TO 099514 PRELIMINARY, PRT: 105 AA.

C 099514 OF 1997 (TREMBLEEL 03, CREATED)

DT 01-MAY-1997 (TREMBLEEL 03, CREATED)

DT 01-MAY-1997 (TREMBLEEL 03, LASET SEQUENCE UPDATE),

DT 01-MAY-1997 (TREMBLEEL 03, LASET SEQUENCE UPDATE),

DT 01-MAY-1997 (TREMBLEEL 07, LASET ANOTATION UPDATE),

DT 01-MAY-1997 (TREMBLEEL 07, LASET ANOTATION UPDATE),

DE LICHT CHAIN FAB FRACKENT (FRACHENT)

OS EDUCATOTA, METALON, CHORDATA, VERTEBRATA, TETRAPON, RAMMALIA),

DE UTHERAIN, PRIMATES.

REQUENCE PROM N.A. 7224 Gaps

SEQUENCE FROM N.A. WING R.G., WINTER G.:
NAT. BIOTPENED: 15:629-631(1997)
EMBL: V13057; E313275;
FFAM: PF00047; 19.
NOW\_TER. 1

NON\_TER 1 1 1 1 1 NON\_TER 244 244 SEQUENCE 244 AA; 26127 MW; A4CF148B CRC32;

Indels

e 12: DB 11; Length 241; L. No. 1.16e-09; Mismatches 0; Indels 0;

Query Match 8.3%; Best Local Similarity 100.0%; Matches 12; Conservative

107 10
100288 PRELIMINARY: PRT: 244 AA.
100288 PRELIMINARY: PRT: 244 AA.
100289 PREMISSION OF CREATED
101-JUL-1997 (TREMBLEEL O4. LAST SEQUENCE UPDATE)
101-JUL-1997 (TREMBLEEL O5. LAST SEQUENCE UPDATE)
101-JUL-1997 (TREMBLEEL O5. JAST SHORMENTON UPDATE)
11NUE-CHAIN FV FRACHENT (FRACHENT).
11NUE-CHAIN FV FRACHENT (FRACHENT).
11NUE-CHAIN FV FRACHENT (FRACHENT).
11NUE-CHAIN FRACHENTON: CHORDATA; VERTEBRATA: TETRAPODA; MANGALIA:
111

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HORE M. P., VOCEL M., BIAGGI C., MIZSCHER S.M., STADLER B.M.;
SUBMITTED (SEP.1996) TO EMPL/GENBANK/DDBJ DATA BANKS.
ETGEL: 708148: 227454; E.M., FANGE C., MIZSCHER B.M.;
FFAM: PPOORAT, 19.
10.1 10.1 10.
NON\_TER 10.5 10.5 10.5 NON\_TER 105 105 SEQUENCE 105 AA; 11303 MW; 24987EC3 CRC32;

Query March 7.6%; Score 11; DB 4; Length 103; Best Local Similarity 100.0%; Pred. No. 1. 49e-07; Matches 11; Conservative 0; Mismatches 0; Indels 0 Gaps

RESULT 13

DESULT 13

RESULT 15

RESULT 15

RESULT 15

RESULT 16

RESULT 15

RESULT 16

Cuery Match 7.6%; Score 11; DB 4: Length 107; Best Local Similarity 100 0%; Pred. No. 1.49e-07; Matches 11; Conservative 0; Mismatches 0; Indels 0

4 MTQSPSSLSAS 14 ||||||||||| 24 MTQSPSSLSAS 34

RESULT 13 ID Q99980 AC Q99980;

Preliminary;

PRT;

107 AA

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O002389 PRELIMINARY: PRT: 240 AA.
0002389;
01-701-1997 (TREMBLERI: 04, CREATED)
01-701-1997 (TREMBLERI: 04, LAST SEQUENCE OFDATE)
01-700-1998 (TREMBLERI: 07, LAST MHOOTATION UPDATE)
SINGLE-CHAIN FY FRAGMENT (FRAGMENT).

KOMO SAPIENS (HUMAN). EULAKYOTA; METAKOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES.

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229 TFGGGTKLEIK 239 ||||||||||| |117 TFGGGTKLEIK 127

01-MAY-1997 (REMAIREL, 03, CREATED)
01-MAY-1997 (REMAIREL, 03, CREATED)
01-MAY-1998 (REMAIREL, 05, LAST SHORDATION UPDATE)
VASOACTIVE INVESTIBAL POLYPEPTIDE HYDROLYZING AUTOANTIBODY LIGHT CHAIN
ROMO SAPIENS (HUMAN).
BUDARYOTA, METRACAA, CHORDATA; VENTEBRATA, TETRAPODA, MANNALIA,
EUTHRETA; PETRATAS.

STIPRE RESERVED TO

PAUL S.;

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

RENNARD S., PAU

TOTOTULKOVA S., GAO Q.S., THOMPSON A., RENNARD S., PAU

BIOCHIM. BIOCHES. ACTA 1116:217-223(1996).

EMBL. 143498; G1850120.

FRAM: PF00047: 19.

1 NON.TER 107 107

NON.TER 107 107

SEQUENCE 107 AA; 11825 MM; C1E164AA CRC32:

Query Match 7.6%; Best Local Similarity 100.0%; Matches 11; Conservative Score 11; DB 4; 1 Pred. No. 1.49e-07 0; Mismatches ( 0; indels Length 107; o, Gaps

0

8

234 TPGGGTKLEIK 244 ||||||||||| |117 TPGGGTKLEIK 127

Query Match 7.6%; Best Local Similarity 100.0%; Matches 11; Conservative

Score 11; DB 4; Length 244; Pred. No. 1.49e-07; O: Mismatches O; Indels

ö

Gaps

NON TER 244 244 SEQUENCE 244 AA; 26025 MW; 47670049 CRC32;

GODDANCE FROM N.A. ZHU Z., CARTEN P.;
GODDANED A., YANN J., ZHU Z., CARTEN P.;
SUBMITTED (FEB-1999) TO ZHOM/GENBANK/DDBU DATA BANKS
EMBL. AF04877. G2911500;
NOW\_TER 244 244
144 244

043699 PRILHINARY; PRT; 244 AA.
043699 PRILHINARY; PRT; 244 AA.
043699 PRILHINARY; PRT; 244 AA.
01-UN-1998 (TREMBLERI, 06, CREATED)
01-UN-1998 (TREMBLERI, 06, LAST SEQUENCE UPDATE)
01-UN-1998 (TREMBLERI, 06, LAST SEQUENCE UPDATE)
NATI-HERB SCPV (FRANCEST).
END SAPIRES (ENDAN):
ENDANOON. METAKOA, CHORDATA; VERTEBRATA; TETRAPODA: MAMMALIA; e
10 HEREAL; PRIMATES.

B 

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RESULT 14

DESCRIPTION OF THE PRECIPITARY: PRT; 239 AA.

AD 24859.

DET 01.301.1988 (TREMBLAREL. 06, CREATED)

DET 01.301.1988 (TREMBLAREL. 06, LAST SEQUENCE UPDATE)

DET 01.301.1988 (TREMBLAREL. 06, LAST ANNOTATION UPDATE)

DE ANTI MEL SCFW (FRACHERY)

OC EUTHERL: PRINATES.

CO EUTHERL: PRINATES.

RE 11

RE 500URNE FROM N. A., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J., ZIU Z., CARTER P.;

RA COEDNAD A., TUAN J.,

Onery Match 7 64; Score 11; DB 4; Length 239; Best Local Similarity 100 0N; Pred. No. 148-07; Matches 11; Conservative 0; Mismatches 0; Indels 0 Caps

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Mon

PRAM: PRODO47: 19.

NOW\_TER 107 107

SEQUENCE 107 AA: 11933 MM; 3BF775AC CRC32:

.. Gaps 0

67 DYSLTISSL 75 ||||||||| 90 DYSLTISSL 98 Score 9; DB 11; Length 99; Pred. No. 1.42e-03; 0; Mismatches 0; Indels 0

RESULT 18 1 ID 014540; AC 014540; DT 01-JAN-1998; DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
(TREMBLREL. 05, LAST SEQUENCE UPDATE) PRELIMINARY; PRT; 113 AA

Query Match 6.9%; Score 10; DB 11; Length 107; Best Local Similarity 100 0%; Prect. No. 161e-05; Matches 10; Conservative 0; Mismatches 0; Indels

70 DYSLTISSLE 79 |||||||||| 90 DYSLTISSLE 99

RESULT 17

IN THE PRICE STATES OF THE PRICE STATES OF AA.

AC 997(09) PRELIMINARY: PRI 99 AA.

AC 997(09) PRELIMINARY: 0, CREATES

DT 01-MAY-1997 (TRENDLEEL: 0) LAST SECREME UPDATE)

DT 01-MAY-1997 (TRENDLEEL: 0) LAST SECREME UPDATE)

DE REGOM (FRAGERY)

DE REGOM (FRAGERY)

OC EMPRICOT: (FRADERY)

OC EMPRICOT: (FRADERY)

OC EMPRICOT: (FRADERY)

OC EMPRICOT: (FRADERY)

AR 121

RP 
Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative

Caps

0

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DE OSSUS 16

ID O3538 PRELIMINARY, PRT: 107 AA.

AC O3538 PRELIMINARY, PRT: 107 AA.

AC O3538 PRELIMINARY, PRT: 107 AA.

AC O3538 PREMILERE. 05, CREATED

DT 01-JAN-198 (TREMBLEEL. 05, LAST ENQUENCE UPDATE)

DT 01-JAN-198 (TREMBLEEL. 05, LAST ENQUENCE UPDATE)

DE RAPPA (FRACHENT).

ON MUS MUSCULUS (MOUSE).

OC EUTANCOA. METACOA; CHORDATA; VERTEBRATA; TETRAPODA: MANNALIA:

OC EUTHERIA, RODENTIA.

RE 11

RE STOLEMET FROM N.A.

RE STOLE

SEMOTENCE FROM N.A.
STRAID-BALB/C:
UDA T., HIFFMI E., ISHIMARU H., HORHHARA F., ITOH T.,
JERMENY. BIOCHG. 83.33.340(1997).
EMEL. D55701; D1024467; ...
EMEL. D55701; D1024479.

01.AUG-1998 (FREMENER). 07, LAST ANNOTATION UPDATE)
HRV FAN 027-Y. (FRAMENT).
HOMO SANTENS (HUMA),
EURAKYOTA, METNIOA, GEORDATA; VERTEBRATA; TETRAPODA
EUTHERIA; PRIAMTES. TETRAPODA; MAMMALIA;

STRREAM

NON\_TER 113 113 SEQUENCE 113 AA; 12383 MW; FCEB1F02 CRC32; SEGUENCE FROM N.A.
TISSUM-PAL.
TITOSUK. SEGURIT T.:
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ
DBBL. ABBO6849: D.1023047; -.
DFAL FROCO47; 5.
DFAL FROCO47; 5.
DFAL FROCO47; 5.
DFAL FROCO47; 5.

Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative Score 9; DB 4; Length 113; Pred. No. 1.42e-03; 0; Mismatches 0; Indels 0; Indels 0 Gaps

5 QMTQSPSSL 13 ||||||||| 23 QMTQSPSSL 31

RESULT 19
ID 01393; PRELHIMARY; PRT: 116 AA.
AC 015983; PRELHIMARY; PRT: 116 AA.
AC 015983; PRELHIMARY; PRT: 116 AA.
DT 01-W07-1996 (TREMBLEEL 01, CREATED)
DT 01-W07-1996 (TREMBLEEL 01, LAST ENGUNNE UPDATE)
DT 01-W07-1996 (TREMBLEEL 01, LAST ENGUNNE)
DE RHEUMANDID PACTOR C6 LIGHT CHAIN (FRAGMENT).

C8 HONO SAPIRS (HUMAN).
C9 EUTHCRIA; PRIMATES.
C9 HONO SAPIRS (HUMAN).
C9 EUTHCRIA; PRIMATES.
RW [1]
RW 121
RW 25002ECE FROM N.A.
RWELTIS RECH (MUNCH.) 36:380-388(1993).
DR 25412; 555183; 395851; .
DR 25412

Query Match 6.2%; Best Local Similarity 100.0%; Matches 9; Conservative Score 9; DB 4; Leng Pred. No. 1.42e-03; 0; Mismatches 0; Length 116; Gaps

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1 DIGHTQSPS 9

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ş 밁 Ouery Match 5.5%; Best Local Similarity 100.0%; Matches 8; Conservative 6 MTQSPSSL 13 Score 8: DB 4: Length 113: Pred. No. 9.71e-02: 0: Mismatches 0: Indels 0; Gaps 0

Apr 19 13:23:54 1999 EQUENCE FROM N.A.

EQUENCE FROM N.A.

TOSIS-PELLINKI T.;

TOSIS-PE US-08-836-455-2.rspt

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RESULT 21

DO 0.45377

PRELIMINARY: PRT: 115 AA.

AC 0.45377

DOT 01-AM-1998 (TREMELREL. 05, CSEATED)
DOT 01-AM-1998 (TREMELREL. 07, LAST ANNOTATION UPDATE)
DOT 01-AM-1998 (TREMELREL. 07, LAST ANNOTATION UPDATE)
DOE HEV PAR NOT-VE (TREMELREL. 07)
COS CONTROLAS (TRAMELREL. 07)
COS CONTROLAS (TRAMELREL 07)
COS CONT
```

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MEDLINE: 97076268. ROCCA A.;
DECONET C. COCKE M., ROCCA A.;
CLIN. EXP. IMMUNOL. 106:357-361(1996).
EMBL: 683599; G1911733; -.
PRAM. PEPOCOGF; 19.
ROM_IER. 1
           NON_TER 134 AA;
1
134
; 14534 MW; 9F908F98 CRC32;
```

10 P

Query Match 5.5%; Best Local Similarity 100.0%; Matches 8: Conservative 122 GTKLEIKR 129 ||||||| 121 GTKLEIKR 128 Score 8: DB 4: Length 134; Pred. No. 9.71e-02; 0; Mismatches 0; Indels 0 Caps 0

RESULT TO SERVICE SERV 035140 PRELIMINARY, PRT: 243 AA.
035140; OSTATED
01-JAN-1998 (TREMBLEEL. OS, CREATED)
01-JAN-1998 (TREMBLEEL. OS, LAST SECOUNCE UPDATE)
01-JAN-1998 (TREMBLEEL. OS, LAST SECOUNCE UPDATE)
01-MOC-1998 (TREMBLEEL. OS, LAST SECOUNCE UPDATE)
MATI-CD10 MOMB KI-4 SCPV (FRAGEET).
MUS MUSCULUS (MOUSE).
EUTHROTH: MCTMLOAL CHORDATH: VERTEBRATA: TETRAPODA: MAMMALIA;
EUTHRETA: NOCESTIA. EGUENCE FROM H. A.

STATE S. MATTHEY B., LEMKE H., ARENDS J.W., DIEHL V.,
KLIMKA, BARTH S. MATTHEY B., LEMKE H., ARENDS J.W., DIEHL V.,
KROCENDOM H. EMBERT A.,
KROCH H. EMBERT A.,
KROCH H. EMBEL S. MATTHEY B.,
KROCH H. EMBEL S. MATTHEY B.,
KROCH H. E.,
KROCH H. S. MATTHEY B.,
KROCH H. S. MATTH

NON\_TER 243 243 SEQUENCE 243 AA: 26225 MW; E0AD5383 CRC32; Match 5.5%;
Local Similarity 100.0%;
es 8; Conservative Score 8; DB 11; Length 243; Pred. No. 9.71e-02; O; Mismatches O; Indels 0 Gaps

RESULT 25 ID 068711 AC 068711; 8 236 GTKLEIKR 243 ||||||| 121 GTKLEIKR 128 PRELIMINARY; PRT; 771 AA. 0

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01-AUG-1998 (TREMBLEEL 07, CREATED)
01-AUG-1998 (TREMBLEEL 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLEEL 07, LAST ANNOTATION UPDATE)
TRIANSPOSASE (TRIO00) HOMOLOG.
TREA.

YERSINIA PESTIS.
PLASHID PESTIS.
PROKANYOTA, GIACILICUTES; SCOTOBACTERIA; PACULTATIVELY
PROKANYOTACIACEAE.
LIVEROBACTERIACEAE.

ANAEROBIC

STOURICE FROM N.A.
STRAIN RIM.
STRAIN RIM.
RIP., ELLIOTT J., MCCREADT P., SKOWRONSKI E.,
RIP., ELLIOTT J., MCCREADT P., SKOWRONSKI E.,
ROCARRANO A.V., BEUGHARER R., GARCIA E.;
SUBMITTED (MRA-1998) TO ZEGL/CENBARK/DDBJ DATA
ENGL: AFOS3946; G2996271; FLASKID.
SEQUENCE 771 AA: 88102 MW; 4D39ABBF CRC32; BANKS. GARNES KOBAYASHI A.,

Query Match 5.5%; Best Local Similarity 100.0%; Matches 8; Conservative Score 8: DB 2: Length 771: Pred. No. 9.71e-02: 0: Mismatches 0: Indels 0 Gaps

밁 323 SLTISSLE 330 |||||||| 92 SLTISSLE 99

RESULTS 36

RESULTS 36

RESULTS 36

RELINIMARY, PRT; 13 AA.

AC 0.18358, PRELINIMARY, PRT; 13 AA.

AC 0.18358, PRELINIMARY, PRT; 13 AA.

AC 0.18358, PRELINIMARY, OF CREATED, OF CREATED, OF CARPO, AC (PROGRAME, 01, ACT SEQUENCE UPDATE), OF CREATED, OT, LAST ANNOTATION UPDATE), OF CREATED, OT, LAST ANNOTATION UPDATE), OR CREATED, METAGOA, CHORDOATA, VERTEBRATA, ITETAPODA, MANGALIA; RILARYOTA, METAGOA, CHORDOATA, VERTEBRATA, ITETAPODA, MANGALIA; RILARYOTA, METAGOA, CHORDOATA, VERTEBRATA, ITETAPODA, MANGALIA; RILARYOTA, METAGOA, CHORDOATA, VERTEBRATA, TETAPODA, MANGALIA; RILARYOTA, METAGOA, CHORDOATA, N., KATAGAA, H., YOSHIDA M.C., RILARYOTA, TAKAYAMA N., KATAGAA, H., YOSHIDA M.C., RILARYOTA, DELICRIMARY, ODBJ DATA BANKS.

PR NOLTER 13 13

SO SEQUENCE 13 AA; 1406 MH; 73CZ1F27 CRC32;

Query Match 4.8%; Score 7: DB 4: Length 13: Best Local Similarity 100.0%; Pred. No. 4.85e+00; Matches 7: Conservative 0: Mimatches 0: Indels

Caps

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Score 8; DB 4; Length 115; Pred. No. 9.71e-02; 0; Mismatches 0; Indels

0

Gaps 0

Query Match 5.5%; Best Local Similarity 100.0%; Matches 8; Conservative 105 GTKLEIKR 112 ||||||| 121 GTKLEIKR 128

RESULT 22

DE 1618 | PRELIMINARY: PRT: 118 AA.

AC 04516 | PRELIMINARY: PRT: 118 AA.

AC 04516 | PRELIMINARY: PRT: 118 AA.

DE 044516 | PRELIMINARY: PRT: 118 AA.

DE 044516 | PREMILEEL. 05; CAST SEQUENCE UPDATE)

DT 01-ANA 1998 ("REMBLEEL. 05; LAST SEQUENCE UPDATE)

DT 04-AC-1998 ("REMBLEEL. 05; LAST ANNOTATION UPDATE)

DE 1804 PAR 1805 HORACHEN;

CONTROLLE REMBLEEL. 05; LAST ANNOTATION UPDATE)

DE 1804 PAR 1805 HORACHEN;

DE 1804 PAR 1805 PAR 1805 HORACHEN VERTEBRATA: TETRAPODA: HA

RE 1804 PAR 1805 PAR 1805 HORACHEN PAR 1805 P

VERTEBRATA; TETRAPODA; MAMMALIA;

Query Match 5.5%; Best Local Similarity 100.0%; Matches 8; Conservative Score 8; DB 4; Length 118; Pred. No. 9.71e-02; 0; Mismatches 0; Indels 0 Gaps

문 108 GTKLEIKR 115 ||||||| 121 GTKLEIKR 128

RP SCHERE RESULT 127 23

OODGS19 PRELIMINARY: PRT: 134 AA.

OODGS19 PRELIMINARY: PRT: 134 AA.

OODGS19 PREMIMERL 04, CREATED;

01-UU-1997 (TREMSLAEL 04, LAST SECTIONE UPDATE)

01-UU-1997 (TREMSLAEL 05, LAST SECTIONE UPDATE)

10-UU-1998 (TREMSLAEL 06, LAST SECTION UPDATE)

REVIS-2 (FRANCHY).

EUGARTON: HENTALON: CHORDATA; VERTEBRATA: TETRAPODA: MAMMALIA;

EUGHERIA: PRIMATES.

SEQUENCE FROM N.A.

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DESCRIPT 31

DO 01594 PRELIMINARY; PRT; 121 AA.

AC 015984; PRELIMINARY; PRT; 121 AA.

DO 01596 (TREDELEEL. 01 CREATED)

DT 01-WOV-1996 (TREDELEEL. 01 LAST SECURNCE UPDATE)

DT 01-WOV-1996 (TREDELEEL. 01 LAST SECURNCE UPDATE)

DE RHEUMATOLD PACTOR 69 LIGHT CHAIN (FRACHENT);

CO CHIPMENA; PRIMATES,

CO ELTHERAN; PRIMATES,

RM 1011NCE FROM A. T.P.

RA ENREL R.W., KENNY T.P.

RA ENREL R.W., KENNY T.P.

RA ENREL R.W., KENNY T.P.

RA ARTHRITS RICHN (MUNCH.) 36:380-388(1993)

DR EMBL: 556194; G29657;

PR PFAM. PERO047.1 19

PR PFAM. PERO047.1 19

TH NOW_TER 121

121

TH NOW_TER 121

121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10

ID 015986 PRELIMINARY: PRT: 118 AA.
AC 015986 PRELIMINARY: PRT: 118 AA.
AC 015986 (PREDBLEEL, 01, CREATED)
DT 01-NOV-1996 (PREDBLEEL, 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (PREDBLEEL, 01, LAST SEQUENCE UPDATE)
DE RIEUMANDID PACTOR D5 LIGHT CHAIN (FRAGMENT).
OS RIEUMANDID PACTOR D5 LIGHT CHAIN (FRAGMENT).
OC EUVARCOTA, MEZHAGA, CHORDATA; VERTEBRATA: TETRAPODA; BA CHORLERA, PRIAATES.
RN (11)
RN SEQUENCE FROM N.A.
RA EHREL R. H., KENNY T. P., CHEN P.P., ROBBINS D.L.;
RN CHARLER N., KENNY T. P., CHEN P.P., ROBBINS D.L.;
RN SEQUENCE SELSP); G39553; .
FT NOW_TER 118
SO SEQUENCE 118 AA: 12766 NN; D2815206 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULY 28
1D 099475, PRELIMINARY: PRT; 110 AA.
AC 099475, OPERATED, 02 COEATED,
DT 01-FEE-1997 (TREMBLEEL 02 COEATED)
DT 01-FEE-1997 (TREMBLEEL 03 COEATED)
DT 01-MCG-1998 (TREMBLEEL 03 COEATED)
DE ANTI-FOLATE BINDING PROTEIN (FRAGMENT).
OS HOMO SAPIENS (EMPLAN).
OC EUNANYOTA: METAKOA: CORDATA; VERTEBRATA: TETRADODA: MAMMALIA:
EN SEQUENCE FROM N.A.
BA WINTER G. CAMPORAR S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 27

ID 03537;

AC 03537;

AC 03537;

PRILIMINARY: PRI: 109 AA.

AC 03537;

DT 01-AN-1998 (TREMSLEEL. 05, CREATED)

DT 01-AN-1998 (TREMSLEEL. 05, LAST SEQUENCE UPDATE)

DT 101-W1998 (TREMSLEEL. 06, LAST ANNOTATION UPDATE)

DL AMEDIA (FRAGMENT)

ON HAMBOA (FRAGMENT).

RE STRAIN-BALE/C;

AR STRAIN-BALE/C;

AR UDA T. HIFURI E. 1581MARU N., MORIMARA F., ITOH T.;

DE PRIL D55659: D0104445;

DR PRIL D56699: D0104465;

DR PRIL D56699: D010469;

DR PRIL D56699: D0104465;

DR PRIL D56699: D0104465;

DR PRIL D56699: D0104465;

DR PRIL D56699: D010469;

DR PRIL D5
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Best Local Similarity 100.0%;
Matches 7: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apr 19 13:23:54 1999
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Best Local Similarity 100.0%;
Matches 7; Conservative
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HOMO SAPIENS (HUMAN).

EUVARYOTA, METAGOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 FGGGTKL 106
||||||||
118 FGGGTKL 124
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|||||||
117 TFGGGTK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 LTISSLE 79
1111111
93 LTISSLE 99
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109
11503 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7: DB 4: Length 118;
Pred. No. 4.85e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7: DB 11; Ler
Pred. No. 4.85e+00;
0: Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-836-455-2.rspt
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RESULT 12

RESULT 12

RESULT 12

RESULT 12

RESULT 13

RESULT 14

RESULT 14

RESULT 14

RESULT 14

RESULT 15

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DE ORSISS PRELIMINARY PRT: 114 AA.

AC 095335 PRELIMINARY PRT: 114 AA.

AC 095335 PRELIMINARY PRT: 114 AA.

AC 095335 PRELIMINARY PRT: 114 AA.

DE ORSISS PREMISER. 02 CENTRE

DE OL-FEE-1997 (FRENDILEEL. 02 LAST ANGOLTON UPDATE)

DE ORNOCLIBERIN (CONLOTROSTS RELEASING ROBONE) (GNRH) (LULIBERIN).

OC EUTHERL SCANCERI (CONNOT PIEZE SIRON)

DE ULARYOTA. METAZOA. CRONDATA: VERTEBRATA: TETRAPODA: MAMOALLA:

RE 11)

RE 11)

RE 12)

RE 12)

RE 12)

RE 12)

RE 13)

RE 14)

RE 14)

RE 15)

RE 15)

RE 15)

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RE 16)

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      RESULT 33 P

ID 048740 P

AC 048740;

DT 01-JUN-1998 (

DT 01-JUN-1998 (

DT 01-AUG-1998 (
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDIRACE PROM N.A.

STOCHAST P.M., MCCREATY P.M., SKOWRONSKI E., ADAMSON A.W.,
LABENZESTEN, MCCREATY P.M., SKOWRONSKI E., ADAMSON A.W.,
BUINEMARY SCHILLER ORDEROUS, TILLE A., RAMIREZ N. STILARGEN S.,
PHAN N. TYLKSCO N. GORNES J. DANAMANA L., POUNDSTONE P.
PHAN NICHT M., ANCONSELLER S., CORPIELD J.U GLANTIX C., ANDREISE T.,
TYLKKELEH M., ANCONSELLER S., CORPIELD J.U GLANTIX C., MONOMERY M.,
BROCE R., THOMAS P., ORDER G., KOMPALLER B., MELLANO M. MONOMERY M.,
ON D., NOLAN M., TRONG S., KOMPANSHI A., OLSEN A.S.,
CHRANTED (MAY-1998) TO EMPLYCENBANK/DDSJ DATA BANKS.

BUBL. ACOMESS; G3108021: ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CANCER RES. 58:991-996(1998).
EMBL: X99990; E265408; -.
FRAM: PF000047; 19:
NON_TER 110 110
SEQUENCE 110 AA: 11392 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 FGGGTKL 106
||||||
118 FGGGTKL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CEN. COMP. ENDOCENIOL. 103:1-13(1996).

POUNTION. STITUMLIES THE SERFICION OF BOTH LUTEINIZING A POUNTION. STITUMLIES HE SECRETION OF CONADOTROPINS. PROSERT, OSSISTATION. SECRETION OF CONADOTROPINS. PROSERT, OSSISTATA;

PROSERT. PROPOSATORN.

PROMETE. PROPATION.

SENDERNEE. MAINTAIN.

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|||||||
118 FGGGTKL 124
                                                                                                                                                                                                                                                                                                                                       9 ILGFLLL 15
|||||||
7 ILGFLLL 13
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|||||||
8 LGFLLLL 14
      G (TREMBLREL. 06, 08)
G (TREMBLREL. 06, 19)
G (TREMBLREL. 07, 19)
                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12897 MW; A7D47B5F CRC32;
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110
; 11392 MW; 761AD54A CRC32;
CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 7; DB 4; Length 158;
Pred. No. 4.85e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7: DB 4: Length 121;
Pred. No. 4.85e+00;
0: Mismatches 0: Indels
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Pred. No. 4.85e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 7: DB 4: Length 110;
Pred. No. 4.85e+00;
0; Mismatches 0; Indels
                                                                                                                                                                158 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-836-455-2.rapt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0:
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Page 42

JUL7 35
001444, PRELIMINARY;
001441, 01-701-1997 (PREMELEEL 04, C)
01-701-1997 (PREMELEEL 04, L)

, CREATED) , LAST SEQU , LAST ANNO

SEQUENCE UPDATE)
ANNOTATION UPDATE) ζ

PRT;

Nenorhabditis elegans. Narvota: Hetazoa: acoelonates: Nexatoda: Secernentea: Rhabditida

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SECUENCE FROM N.A.
SINN P., BUENLER E., DEWAR K., FENG J., KIN C., LI Y., SUN H.,
CONNAY A., CONNAY A., KUNTE D., ONI O., SHEN Y.K., TORINGI N.,
VISCOTSANA V., YU G., DAVIS R.H., FEDERSPIEL N.A., THEOLOGIS A.,
FOYEGO N.
                                                                                                                                                                                                                                                                                                                              P21B7.10.
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EULARYOTA: PLANTA: EMBRYOPHTTA; ANGIOSPERMAE;
CAPPARALES: CRUCIFERAE.
CERER J.R.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AC002560; G2809241;
SEQUENCE 158 AA; 17843 MW; 9074E316 CRC32;
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Query Match

Best Local Similarity 100.0%;
Matches 7; Conservative 70 PSSLSAS 76 ||||||| 28 PSSLSAS 34 Score 7; DB 10; Length 158; Pred. No. 4.85e+00; 0; Mismatches 0; Indels 0

> Caps 0

SEQUENCE FROM N.A.

SERAIN-BRASSON R., ANDERSON R., BAYNES C., BERKS H., BONFIELD J.,

A WILLSON R., ANISCOUGH R., ANDERSON R., DAYNES C., DERKS H., BONFIELD J.,

A BURYN J. CONNELL H., COPSET T., COOPER J., COLLSON B., CRAXTON H.,

A BURYN J., DU Z., DUGBIN R., FAVELLO A., FULTON L., GARDERR A., GREEN P.,

BA MARKES J., HILLER H., JURNSON M., TORNESON M., TORNESON M.,

BA MARKES J., HILLER H., JURNSON M., PARSON J., PRESENT J.,

BA MARKES J., BONES M., DOMALDANN H., BANDON M., SETTH A.,

BA MARKES J., SPLANEN R., SPLEATON J., THIERRY H.EG. J., TROMAS K.,

BA MODERN M., MAGRAIN K., MATESON R., WATSON A., MEINSTOCK L.,

PA MODERN M., WAGHAN K., MATESON R., WATSON A., MEINSTOCK L.,

PA MODERN M., WAGHAN K., MATESON R., WATSON A., MEINSTOCK L.,

PA MODERN M., WAGHAN K., MATESON R., WATSON A., MEINSTOCK L.,

PA MODERN M., WAGHAN K., MATESON R., WATSON A., MEINSTOCK L.,

PA MODERN M., WAGHAN K., WATESON R., WATSON A., MEINSTOCK L.,

PA MODERN M., WAGHAN K., WATESON R., WATSON A., MEINSTOCK L.,

PA MODERN M., WAGHAN K., WATESON R., WATSON A., MEINSTOCK L.,

PA MODERN M., WAGHAN K., WATESON R., WATSON A., MEINSTOCK L.,

PA MODERN M., WAGHAN K., WATESON R., WATSON A., MEINSTOCK L.,

PA MODERN M., WAGHAN K., WATESON A., WATSON A., MEINSTOCK L.,

PA MODERN M., WAGHAN K., WATESON A., WATSON A., MEINSTOCK L.,

PA MODERN M., WAGHAN K., WATESON A., WATSON A., MEINSTOCK L.,

PA MODERN M., WAGHAN K., WATESON A., WATSON A., MEINSTOCK L.,

PA MODERN M., WATESON M., WATESON A., WATSON A., MEINSTOCK L.,

PA MODERN M., WATESON M., WATESON A., WATESON M., WATESO

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8 B
159 LEIKRAD 165
||||||||
|124 LEIKRAD 130
                       Indels
                      0
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RESULT. 34

ID 065725;

PRELIMINATE: PRI: 186 AA.

AC 057755;

DT 01-MG-1998 (TREMBLREL 07; CREATED)

DT 01-MG-1998 (TREMBLREL 07; LAST SADORNICE UPDATE)

DT 01-MG-1998 (TREMBLREL 07; LAST SADORNICE UPDATE)

DE PUTATIVE DECOXYCTYIDYLATE DEMINASE (FRAGMENT).

OC CUTARYOTA: PLANTA; EMBRYOPHTA: ANGIOSPERME: DICOTYLEDONEAE: FABA

CO FUTARYOTA: PLANTA; EMBRYOPHTA: ANGIOSPERME: DICOTYLEDONEAE: FABA

RE 110-ENEME PROM N.A.

RY 205809-TIOLARED PROCOTY: STRAIN-CV. CASTELLAN:

RY 205809-TIOLARED PROCOTY: STRAIN-CV. CASTE
Query Match 4.8%;
Best Local Similarity 100.0%;
Matches 7; Conservative
Score 7; DB 10; Ler
Pred. No. 4.85e+00;
0; Mismatches 0;
                                                                                                                                                      Length 186;
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Apr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-UNY-1999 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
HYPOTHETICAL 31.0 KD PROTEIN.
SLR0041.
MEDLINE 96127539.

MARENO T. TANANA A., SATO S., KOTANI H., SAZUK SUCHEM, M., TANATA S.;

SUCHEM, M., TANATA S.;

DAN RES. 27.157-166(1995).

EMBL. D64005 (20011)7.

EMBL. D6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYNECHOCYSTIS SP.
PROKARYOTA; BACTERIA; GRACILICUTES; OXYPHOTOBACTERIA; CYANOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                  SAZUKA T., MIYAJIMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-836-455-2.rspt
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Overy Match 4.8%; Score 7; DB 2; Length 280; Best Local Similarity 100.0%; Pred. No. 4.85e+00; Matches 7; Conservative 0; Mismatches 0; Indels Indels 0

36 ILGFLLL 42 |||||||| 7 ILGFLLL 13

ID 084144
AC 084144
D7 01-80V-1
D7 01-80V-01-NOV-1996 (TREMBLEEL 01: CREATED)
01-NOV-1996 (TREMBLEEL 01: LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLEEL 01: LAST ANNOTATION UPDATE)
SIGNA C PROTEIN UNKNOWN.
UNKNOWN.
UNKNOWN.
UNKNOWN.
UNKNOWN.
UNKNOWN.
UNKNOWN. PRELIMINARY; PRT: 326 AA. ORTHOREOVIRUS.

Query Ma Best Loc Matches ray Match
Propose 7. J
Ref. Wood Similarity 100 09; When No. 4
Ref. Wood Similarity 100 09; When No. 4
Ref. Wood Similarity 100; When No. 4
Ref. Wood Similarit SEDURNCE FROM N.A.
STRAIN-AVIAN REDVIRUS RAM-1;
STRAIN-AVIAN REDVIRUS I.H.;
KOOL D.A., HOLMES I.H.;
KOOL D.A., HOLMES I.H.;
TO EMEL, CARLAGEMBANK, DDBJ DATA
SUBMITITED DEC 1994; TO EMEL, GENBANK, DDBJ DATA
EMEL, L18502; 6501939; T.
SEDURECE 336 AA; 3500 FM; 45832573 CRC12; ) TO EMBL/GENBANK/DDBJ DATA BANKS DB 14; Length 326; 4.85e+00;

g

140 LTISSLE 146

0; Indels

0

Page

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LISSIE 99

Mon

RESULT ID QS AC Q5 DT 01

ULT 36 Q55461 PRELIMINARY; Q55461; Q1-NOV-1996 (TREMBLREL, /

PRELIMINARY;

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CREATED) PRT; B

9 SPSSLSA 15 |||||||| 27 SPSSLSA 33

Query Match 4.8%; Score 7; DB 5; Length 212; Best Local Similarity 100.0%; Pred. No. 4.85+00; Matches 7; Conservative 0; Mimatches 0; Indels

0 Gaps SEQUENCE PROM N.A.
STRAIN-BRISTOL H3:
MATERSTON R.:
MATERS

OURNE FROM N.A. TRAIN-PRISTOL N2; ZISEL C., WAMSLET P.; PRITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS

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RESULT 18

ID 08391.

AC 08391.

DT 01-NOV-1996 (TREDGLEEL. 01. CREATED)

DT 01-NOV-1996 (TREDGLEEL. 01. LAST SEQUENCE UPDATE)

DT 01-NOV-1996 (TREDGLEEL. 01. LAST SEQUENCE UPDATE)

DE HYDCHIETCAL 15.0 KD PROTEIN.

OS ORTHOREDVIRUS \$1.

OS ORTHOREDVIRUS \$1.

CVIRLINE: DS-RNA NONENVELOPED VIRUSES: REQVIRIDAE.

RN 111

RC STRAIN-SOMERVILLE 4;

RC Query Match 4.8%; Best Local Similarity 100.0%; Matches 7; Conservative SEQUENCE FROM N.A.
STRAIN-SOMEWRILE 4;
ROOL D.A., BOLMES I H.;
SUBMITTED (MAY-1993) TO MOBIL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (MAY-1993) TO MOBIL/GENBANK/DDBJ DATA BANKS.
BEBL., LOTOSEN
KYPOTMETICAL POTERN
ENDOMERICE JS AA; 39971 NH; Z4114E7D CRC32; 140 LTISSLE 146 |||||||| 93 LTISSLE 99 Score 7; DB 14; Len Pred. No. 4.85e+00; 0; Mismatches 0; Length 326 9

RESULT. 39
ID 03225; PRELIMINARY;
AC 03225; PRELIMINARY;
DT 01-NA:1998 (TREMELEZI. 05, CI
DT 01-NA:1998 (TREMELEZI. 05, CI
DT 01-NA:1998 (TREMELEZI. 05, CI
DT 01-NA:1998 (TREMELEZI. 07, LI
DT 01-NA:1998 (TREMELEZI. 07, LI
DE YRBQ PROTEZIN.
DE PROTELLISS
OF PROTELLISS CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE) PRT;

NCÍLIUS SUBTILIS. QUARYOTA: FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE

TOLENCE FROM N.A.

TOLENCE FROM N.A.

TOLENCE OF TOLENCE FROM N.A.

EXPERDO V. BESTETON M.G., BESSIERES P., BOLOTIN A. B., BORCHERT S.,

EXPERDO V., BESTETON M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,

BOUTLET S., BOURSIER L., BRANS A., BRAUM M., BRIGHELL S.C., BRON S.,

ROUTLET S., BROSSHI C.V., CALDMELL B., CAPAINON V., CARTER M.M.,

BOIS.K., CODANI J.J., CONNERCON I.P., COMMINGS N.J., DANIEL R.A.

BILOT F., BOYDER K.M., DONIERBOOF N., ERRLICH S.D., EMBERGON P.T.,

BILOT F., DOYDER K.M., DONIERBOOF N., ERRLICH S.D., EMBERGON P.T.,

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Mon

AN EMPILIA K.D. BERINGTON J. PARRET C. FERMARI E., POULGER D., PRITZ C.,

AN GLASER P. GOPPEND A. GOLGERIU G. STATA A. GALLERON W., SCHAR S. K.

AN GUN B.J. MARA K., MITCH J. MINGOD C. RAMBERG T. GORGER B.,

AN GUN B.J. MARA K., MITCH J. MINGOD C. RAMBERG T. GORGER B.,

AN HOLSAPPEL S., ROSONO S. RULLO M.F. LTANA M. JONES J., HILDER B.,

AN HOLTER P., KONINGETEIN G., KROCH S., KUMANO M. KURITA K. ADTONS A.

KOTTER P., KONINGETEIN G., KROCH S., KUMANO M., KURITA K. ADTONS A.

KOTTER P., KONINGETEIN G., KROCH S., KUMANO M., KURITA K. ADTONS A.

KOTTER P., KONINGETEIN G., KROCH S., KUMANO M., KURITA K. ADTONS A.

KOTTER P., KONINGETEIN G., KROCH S., KUMANO M., KURITA K., ADTONS A.

KONINGER S., MARCH S., MEDICOT C., MEDIKNA M., MELLANO R.P., MITONO M.,

MARION S., MARCH S., MEDICOT C., MEDIKNA M., MELLANO R.P., MITONO M.,

MARION S., MARCH S., MEDICOT C., MEDIKNA M., MELLANO R.P., MITONO M.,

MARION S., MARCH S., MEDICOT C., MEDIKNA M., MELLANO R.P., MITONO M.,

MARION S., MARCH S., MEDICOT C., MEDIKNA M., MELLANO R.P., MITONO M.,

MARCH S., MARCH S., MEDICOT S., MEDICOT C., MEDICOT C

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RESULT 44

ID P78834 PRELIMINAT; PRT; 444 AA.

AC P78834 PRELIMINAT; PRT; 444 AA.

DT 01-MAY 1997 (TREMBLEEL 03 CREATED)

DT 01-MAY 1998 (TREMBLEEL 05 LAST REQUENCE UPDATE)

DT 01-MAY 1998 (TREMBLEEL 05 LAST REQUENCE UPDATE)

DE FISSION YEAST (FRAGMENT). LAST ANOTATION UPDATE)

OS SCHILORACCHARONICES POMER (FISSION YEAST).

OC EMARYOTA: FUNGI: ASCOMYCOTINA; HEMIASCOMYCETES.

RN (1)

RN 1574ALPROPERS.

RN CSPHALPROPESS. ASCOMYCOTINA; HEMIASCOMYCETES.

RN TOSHIJORA S., MAYO K., NAKAI K., OKAYAMA H., NOJIMA

RN DEALE, B801373; D104531; ...

DR MAY BREWL, D801373; D104531; ...

DR MAY BREWL, D801373; D104531; ...

DR MAY BROOKS (TRAMBECOLABE).

FE NOW 1787 P00455; TRAMBECOLABE.

FOR NOW 1787 P00455; TRAMBECOLABE.

FOR NOW 1787 P00455; TRAMBECOLABE. Mon RESULT 41

ID 001833 PR
AC 001833 PR
AC 001831 PR
AC 0018 Ş 8 DR RARARA RARARA Ouery Match 4.8%; Score 7; DB 3; Leng Best Local Similarity 100.0%; Pred. No. 4.85e+00; Matches 7; Conservative 0; Mismatches 0; λpr Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative DI SEGURNOE PROM N. A.

RESTATMENDISTON HELD M., ANDERSON K., BANNES C., BERKS M., BONFIELD J.,

AN HILSON H., ANDECOGH R., ANDERSON K., BANNES C., BERKS M., BONFIELD J.,

AN HANKINS T., HILLIER L., JUER M., JOHNTON L., CARDINER, GREEN P.,

AN HANKINS T., HILLIER L., JIER M., JOHNTON L., DANS M., CORTINGE B., O'CALLAGRAN M., PARSONS J., DERCY

AN HONORAY A., MORTHONE B., O'CALLAGRAN M., PARSONS J., DERCY

C. A. RIKEN L., ROOPRA M., ANDERSON J., SHOPMINER R., SALLON M., SHIH A.,

ROUNDAMERS E., SPACES R., BULSTON J., THIERKY-HIED J., THOMAS K.,

A SOUNDAMERS E., SPACES R., BULSTON J., THIERKY-HIED J., THOMAS K.,

A SOUNDAMERS E., SPACES R., BULSTON J., THIERKY-HIED J., THOMAS K.,

A MILLIESON SHOUGHAM K., WATERSOYDE R., WATERSOYDE R., BALLON M.,

AN HILLIESON SHOUGHAM K., WATERSOYDE R., WATERSOYDE R.,

AN HILLIESON SHOUGHAM K., WATERSOYDE R., WATERSOYDE R.,

AN HILLIESON SHOUGHAM K., 
AN HILLIE Query Match SEQUENCE PROM N.A.

STRAINERS, 45.

STRAINERS, 45.

DAG RES. 4.56.

SEGUENCE S. AATO K., NAKAI K., OKAYAMA H., NOJ

DAG RES. 4.56.

DAG RES. 4 368 GGTKLEI 374 |||||||| |120 GGTKLEI 126 Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative STURKTYED (PEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: ABOOSSIS: D1024758: .
EMBL: ABOOSSIS: D1024758: .
EMBL: ABOOSSIS: D10245748: .
SEQUENCE 440 AA: 4919 MM; 876183B1 CRC32; AMANAMAYASIY, SAMADA H., HORIKAMA H., HIRAMA Y., HIMO Y., YAMADOO S., SERIHE M., BARA S., KOSIGI H., HOROYAMA A., MCAI Y., SANAI M., OCHOA K., YAMADAMI H., TAMAHTA H., OHURU Y., FUNAHASHI T., YAMAKA T., KUCOH Y., YAMADAMI J., KUSHIDA H., OGUCHI A., OGLI K., YOSHIZAMA T., NAKAURAKA Y., MASUCHI Y., SHIZOYA H., OGUCHI A., KINCHE H., OGURA K., OTSUEA R., MAKAMAN H., FUNNHASHI T., TANAKA T., KUDOH TANAKAKI J., KUSHIDA H., OGUCHI A., YOSHIKANA T., AOKI K., MAKAMURA Y., KANAKARAYKSI Y., KIKUCHI H.; SUBHITTED (JUN-1997) TO EMBL/GEMBANK/DDBJ DATA BANKS. 19 13:23:54 1999 SEQUENCE FROM N.A.
STRAIN-BRISTOK N:
STRAIN-BRISTOK N:
BLANCHARD M., MANSLEY P.;
BLANCHARD M., MANSLEY P.;
BLANCHARD M., MANSLEY P.;
BLANCHARD M., MANSLEY P.;
BLANCHARD GRAVINIST GLAVOLES;
BLANCHARD GLAVOLES;
SEQUENCE 416 AA; 46619 MM; CJ7D3BOA CRC32; 188 LGFLLLL 194 ||||||| 8 LGFLLLL 14 ESDITENCE PROM N.A.
O'DOND B.F., NGUTEN T., MARCHESE A.,
O'DOND B.F., NGUTEN T., CEDORGE S.R.,
ROLAKOWSLI L.F. JR., GEDORGE S.R.,
ENGLAKOWSLS, GAT19105;
SEGURACE 379 AA: 40036 NF; A232DI enorhablitis elegans. Tartota: Metazoa: acoelohates; Nekatoda: Secernentea; Rhabditida. ZENCE FROM N.A. (TREMBLREL.)
(TREMBLREL.) Preliminary; 4.8%; 922 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE) Score 7; DB 1; Length 440; Pred. No. 4.85e+00; O; Mismatches O; Indels Score 7; CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE) Score 7; DB 11; Length 379; Pred. No. 4.85e+00; 0; Mismatches 0; Indels PRT; A232DB39 CRC32; DB 5; CHENG 416 AA. H., NOJIMA US-08-836-455-2.rspt Length 444; R., LYNCH K.R., Length 416; 0 0 HENG H.H.Q., Gaps Gaps

19 13:23:54 1995

Mon

Apr

RESULT 40

ID 054897 PRELIMINARY: PRT; 379 AA.

AC 054897, PRELIMINARY: PRT; 379 AA.

PT 01-UN-1598 (TREMBLEREL, 06, CARATED)

DT 01-UN-1598 (TREMBLEREL, 06, LAST SEQUENCE UPDATE)

DT 01-UN-1598 (TREMBLEREL, 06, LAST ANNOTATION UPDATE)

DR 0 PROTEIN COUPLED RECEPTOR.

GN 0PR 27. NOSCULUS (MOUSE).

OC EVERATORIA. ROTERTIA.

NÚS MÚSCULUS (MOUSE). EULARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMALIA; EUTHERIA; RODENTIA.

Ş B

39 SLSASIG 45 |||||||| 30 SLSASIG 36

Query Match 4.8%; Score 7; DB 2; Length 340; Best Local Similarity 100.0%; Pred. No. 4.85e+00; Matches 7; Conservative 0; Hismatches 0; Indels

Indels

0

Gaps

SOUTHAND FROM N.A.
SENAIN-68; CARANARA N., YOSHIKAWA H., DANCHIN A.;
KUNST F., OGARAWARA N., YOSHIKAWA H., DANCHIN A.;
KUNST F., OGARAWARA N., YOSHIKAWA H., DANCHIN A.;
SUMMITTED (NOV-1991) TO EMBLYGENBANK/DDBJ DATA BANKS.
EMBL: ES9121; E118668; C.
SEQUENCE 340 AA; 37382 MM; 65C1FE2D CRC12;

US-08-836-455-2.rspt

Best Local Similarity 100.0%; Matches 7; Conservative O; No. 4.85e+00; Mismatches 0; Indels 0;

Caps

RESOLT
AC 044
AC 044
AC 041
AC

SEQUENCE FROM N.A. STRAIN-972H-;

WOOD Y DAIMEDRAM M.A. BARRELL B.G., HAMLIN M., CHUNCHER C.M.;
SUBMITITED (FEB-1998) TO SUCCEENANK/DDB-JDATA BARKS.
BRDL: ALO21818, ELIZ51100.
SUBMITITED (FEB-07EIM).
KTPOTTETICL, PROTEIM.
SEQUENCE 421 AA: 47663 MM; OC2631E8 CRC32;

Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative Score 7; DB 3; Pred. No. 4.85e+ 0; Mismatches DB 3: Length 421; . 4.85e+00; matches 0: Indels

0

Gaps

0

348 QSPSSLS 354 ||||||| 26 QSPSSLS 32

RESULT 43

ID 050114 PRELIMINARY: PRT: 440 AA.

AC 050114 PRELIMINARY: PRT: 440 AA.

AC 050114 PRELIMINARY: PRT: 440 AA.

DT 01-UNN-1998 (TREMBLERL. 06, CAST SEQUENCE UPDATE)

DT 01-WG-1998 (TREMBLERL. 07, CAST ANNOTATION UPDATE)

DT 01-WG-1998 (TREMBLERL. 07, CAST ANNOTATION UPDATE)

DE 104-WG-1998 (TREMBLERL. 07, CAST ANNOTATION UPDATE)

DE 104-WG-1998 (TREMBLERL. 07, CAST ANNOTATION UPDATE)

REVERTABLE DEFERRED AND A.

REVERTABLE DEFERRED A. A.

REVERTABLE DEFERRED A. A.

REVERTABLE DEFERRED A. A.

REVERTABLE AND A. A. MAGAI Y., SANDAN M., HAIKAMA Y., HINO Y., SPANDA B. A. SEKIER M. B.BAS S., ROSUUI H., HOSOYAMA A., NAGAI Y., SI

THERMOCOCCACEAE; PYROCOCCUS

SECUENCE FROM N.A.
STRAIN-OT):
OHTUTU T., HORIKAWA H., SAWADA M., HAIKAWA Y., HINO Y., YAMAHOTO S.,
SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NACAI Y., SAKAI M.,

...

Page 47

Indels 0 Gaps

0

Page ŧ

162 PPSSKLG 168

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US-08-836-455-2.rspt

RESULT 45

ID 046120;
AC 046120;
AC 046120;
DT 01-WW-1996 (TREMELREL 01, CR 07 01-WW-1996 (TREMELREL 07, LA DT 01-WW-1997) TO STEALE FROM B. A. HENDERSON J. WW-1997) TO STEALE A. HENDERSON J. WW-1997) TO STEAL MPYLOBACTER JEJUNI. ROKARYOTA: GRACILICUTES: SCOTOBACTERIA: ROBIC, MOTILE, HELICAL AND/OR VIBRIOID PPSSKIG 145 EMBL/GENBANK/DDBJ DATA BANKS. CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE) PRT; 472 ۶

PROTEASE. SEQUENCE 472 AA; 50940 MW; 6CBCA101 CRC32;

Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative Score 7: DB 2: Length 472; Pred. No. 4.85e+00; 0; Mismatches 0; Indels 0; Indels

0

Gaps 9

ĝ 101 SSLGSGV 107 ||||||| 72 SSLGSGV 78

PRT;

RESULT 46

ID 035161 PRELIMINAN: PR
AC 035161; PREMILEEL 05, CREA
DT 01-JAN-1998 (TREMBLEEL 05, LOTE
DT 01-JAN-1998 (TREMBLEEL 07, LAST
DT 01-JAN-1998 (TREMBLEEL 07, LAST
DT 01-JAC-1998 (TREMBLEEL 07, LAST
DE SEVEN TRANSMEMBRANE RECEPTOR.
G. CELSH.
G. CELSH.
G. CELSH.
G. CELSH.
G. CELSH.
G. GETHRACH, RODEWITA.
RM (11UMERIA; RODEWITA.
RM (11UMERIA; RODEWITA.
RM SEDURACE PROM N. 1.
RM SEDURACE PROM N. A. , SHEWARD M. J.
RA HALJANTONAKIS AR., SHEWARD M. J. CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE) VERTEBRATA; TETRAPODA; MAMMALIA;

SÉQUENCE FROM N.A. STRAIN-C57/ALG: TISUS-BRAIN: STRAIN-C57/ALG: 7180720. HADJANTONAKIS A.K., SHEWARD W.J., HARMAR A.J., DE GALÂN L.,

Apr 19 13:23:54

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IREILLE P., DEADMAN R.; BMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA

SEQUENCE FROM N.A.
STRAIN-BRISTOL N.;
WATESTON N.;
WATESTON N.;
GIDNITTED (NOV-1996) TO EMEL/GENBANK/DDBJ DATA BANKS.
EMEL USGG51, DNAJL; 1 1PROSITE: PSGG56, DNAJL; 1FRAN; PFG0725; DNAJ, 67122 NN;
SEQUENCE S91 AA; 67122 NN;
SEQUENCE S91 AA; 67122 NN;

F Obery Match 4.8% | Secore 7, DB 5, La Best Local Schilarity 100,00; Pred No. 4.85+00; Matches 7; Conservative (%) Mismatches b) 23 VSLTCBA 229 Length 591; 0; 'Indels ç, Caps

CURARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA

STRAIN-BRISTOUR;
STRAIN

RAIN-BRISTOL N2

Page 51

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877777777778

SECOUNCE FROM N.A.
STRAIN-IOWA FIELD; TISSUE-LEAP;
STRAIN-IOWA FIELD; TISSUE-LEAP;
MODDMORTH A.R., ROSEN B.A., BERNASCONI P.;
PLANT PHYSIOL, 111:1153-1153(1997).
EMEL, USSES; G111482; ...
PFAM; PF00205; TPP\_ensymes.

1 91 569 665 **A**A; 90 P 665 A 569 L POTENTIAL.
ACETOLACTATE SYNTHASE.
L -> W.
L -> W.
AAA3D860 CRC32;

Query Match 4.8%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 10; Len Pred. No. 4.85e+00; 0; Mismatches 0; Length 665; 0

밁 64 TQSPSSL 70 |||||||| 25 TQSPSSL 31

RESULT SO

DESCRIPT SO

O27451

PRELIMINARY, PRT: 684 AA.

AC 027451

DT 01:MOV-1996 (TREMBLHEL. 01, CARATED)

DT 01:MOV-1996 (TREMBLHEL. 02, LAST SHORENCE UPDATE)

DT 01:MOV-1996 (TREMBLHEL. 03, LAST SHORENCE UPDATE)

DT 01:MOV-1996 (TREMBLHEL. 04, CAST SHORENCE UPDATE)

DE (TREMBLHEL)

DE (TREMBLHEL

Query Match 4.8%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 5; Length 684; Pred. No. 4.85e+00; 0; Mismatches 0; Indels

0

GAPS

0

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Page 50

HOOVERS J. H. H., LITTLE P. P. R.;
CENONICS 41:97-104(1997).
CENONICS 41:97-104(1997).
TRAISISTEMBALE.
FRANSIZEMBALE.
SEQUENCE 501 AA; 54331 NN; 8231802E CRC32;

Query Match 4.8%; Score 7; DB 11; Len Best Local Similarity 100,0%; Pred. No. 4,85e400; Matches 7; Conservative 0; Mismatches 0; Length 501;

Indels 0 Gaps

449 TSSLGSG 455 |||||||| 71 TSSLGSG 77

RICKETTSIALES;

RESULT 47

ID 045913 PRELIMINARY; PRT; 526 AA.
AC 045913 PREMISSER. 01. CREATED)
DT 01.40V-1996 (PREMISSER. 01. LAST SEQUENCE UPDATE)
DT 01.40V-1996 (PREMISSER. 01. LAST SEQUENCE UPDATE)
DE 08F 276.
OR 276.
OR 276.
PROMANYOTA: GRACILICUTES: SCOTOBACTERIA: RICKETTSIACEAE.
OC RICKETTSIACEAE.
RY (1)
RP SEQUENCE FROM N.A.
RY STRAINFWINGS H., THELE D., VALCOVA D.;
RR STRAINFWINGS H., THELE D., VALCOVA D.;
STRAINFWINGS H., THELE D., VALCOVA D.;
STRAINFWINGS H., THELE D., VALCOVA D.;
STRAINFWINGS H., THELE D., VALCOVA D.;
STRAINFWINGS H., THELE D., VALCOVA D.;
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STRAINFWINGS H., THELE D., VALCOVA D.;
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STRAINFWINGS H., THELE D., VALCOVA D.;
STRA

Ouery Match 4.8%; Score 7; DB 2; Langth 526; Best Local Similarity 100.0%; Pred. No. 4.85e+00; Additional Matches 7; Conservative 0; Mismatches 0; Indels 0 Gaps

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븅 485 85LSASL 491 |||||||| 29 85LSASL 35

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RESULT 48

ID 991243 PRELIMINARY; PRT: 591 AA.

AC 991243 PRELIMINARY; PRT: 591 AA.

AC 991243 PRELIMINARY; PRT: 591 AA.

DT 01-MAY-1997 (TREMBLEEL 03, CREATED)

DT 01-MAY-1997 (TREMBLEEL 07, LAST SEQUENCE UPDATE)

DT 01-MAY-1998 (TREMBLEEL 07, LAST ANOTATION UPDATE)

DE SIMILARIT TO A DINN-LIKE DOMAIN.

OS CARROWINDITIS ELECANS.

US-08-836-455-2.rspt

Mon Apr 19 13:23:54 1999 Db 201 DIGINLH 207 |||||||| Cy 48 DIGINLH 54 Search completed: Thu Apr 15 18:04:57 1999 Job time : 71 secs. US-08-836-455-2.rapt i Page 53

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GENESEON: T58328
GENESEON: T13270
GENESEON: T73578
GENESEON: T58327
GENESEON: T90986
GENESEON: 779930
GENESEON: V09805
GENESEON: V09805
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GENESEQN: V18557
GENESEQN: T36316
GENESEQN: T70868
GENESEQN: N70971
                          GENESEON: 023863
GENESEON: 023862
GENESEON: 023861
GENESEON: 023859
GENESEON: 023859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENESEQN: V11399
GENESEQN: Q38877
GENESEQN: T85854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENESEQN:T15802
GENESEQN:T88129
GENESEQN:V00687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENESEQN:T77137
GENESEQN:T05312
GENESEQN:T77139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENESEQN: V01097
GENESEQN: Q39234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENESEQN:T39557
GENESEQN:T69541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENESEQN: N91820
GENESEQN: Q32778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENESEQN:Q12637
GENESEQN:V54863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENESEQN: Q65631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENESEQN:T87815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENESEQN: V56413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENESEQN: Q04695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENESEQN: N91146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Geneseq-NA, Release 34.4, Released on 4Feb1999, Formatted on 5Feb1999

word-size: 15 Words: 70791 Diagonals: 2,313 Total-Chagophis: 409,502,538

Integral-width: 1 Alphabet: 4 List-size: 50 CPU minutes: 30.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROMIG of: /home/obryen/ree455/ol1g/US08836455.seq
sequence 3, application us/08836455
general information:
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applicant: foon, kenneth a.
applicant: chatterjee, sunil k.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diag Score Width Documentation ...
Heavy chain variable region of mouse GMP-140 MAb heavy chain coding sequen Human CD30 binding protein cDMA. Poly CTMO1 VH CDNA. Anti-human milk fat gl Anti-Humfe MAb CTMO1 heavy chain varia Ber-H2 heavy gammal chain. DNA mols. Mucin-type synthetic glycolipid antil Fv(GP-2) immunosupreesive. Immunosupreesive. Immunosupreerle heavy chain but molectide sequence of the heavy chain Nucleotide sequence of the heavy chain anti-tobacco mosaic virus monoclonal DNA encoding the heavy chain of the VH186 region of anti-nitrophenylacety scFvB18 construct mutant #5. Producin ScFvB18 construct mutant #4. Producin ScFvB18 construct mutant #4. Producin ScFvB18 construct mutant #3. Producin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine monoclonal anti-idiotype antib 2H7 Vh sequence, Polynucleotide(s) en Coding sequence for heavy chain variat Mouse 2H7 antibody heavy chain variable region heavy chain variable region heavy chain stribed; New Treating B Murine variable region heavy chain fivector contg. TCAE 8 DNA. Treating B Anti-influenza NIO scFv. New target-b MAB VILTEG heavy chain (specific for Heavy chain of monoclonal antibody 6A Sequence encoding the heavy chain variable domain of human Monoclonal antibody of the man of the sequence encoding the deavy chain variable domain of human Monoclonal antibody of the man of the sequence encoding the deavy chain variable domain of human Monoclonal antibody of the man of the sequence encoding the man of the ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibody OK3T heavy chain Murine antibody ICR-1.1 heavy chain I Murine ICR-1.1 V-H region PCR product DNA sequence of the V and J regions G Heavy chain variable region of anti-p Variable heavy chain chain colon for anti-hu Anti-human Fasi antibody (NOK5) heavy Single chain antigen hybrid receptor MAD SCH94.03 heavy chain DNA. Monocld Single chain antigen hybrid receptor L12 MAD VH region DNA. Chimeric and H Variable heavy chain of MAD L12 DNA. Fusion gene sequence encoding anti-Ta Antibody 7612 heavy chain variable region DNA. Chimeric and H Variable heavy chain of MAD L12 DNA.
                              construct mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         check: 9532 from
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U. Distribution rights by Oxford Molecular Ltd n.a. database search, using Smith-Waterman algorithm . K

9: >US-08-836-455-3 (1-461) from US08836455. Sat Apr 17 17:39:43 1999; MasPar . 896.605 time 69.95 Seconds 5 Million cell updates/sec

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Title: Description: Perfect Score: N.A. Sequence: Comp: Scoring table: Gap 60 161) from USO8836455.seq
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REGULT  REGULT  AC N91146  AC N91246  DT 06-3UL-1990 (first entry)  DT 06-3UL-1990 (first entry)  DT 06-3UL-1990 (first entry)  ENT Not acquence.  ENT Antibodies: passive immunisation: pH3-6a; ss.  Synthetic. Location/Qualifiers  FT cds //tug- ENT 039458  FT misc_feature 399458  FT misc_feature 399400  FT misc_feature 399400  FT w0890999-A. //cote-'Sequence homologous to DSP.2'  FT w0890099-A. //cote-'Sequence homologous to DSP.2'  FT w089009-A. //cote-'Sequence homologous to DSP.2'  FT w0890099-A. //cote-'Sequence homologous to DSP.2'  FT w0890099-A. //cote-'Sequence homologous to DSP.2'  FT w0890099-A. //cote-'Sequence homol	The state of the s	961 962 963 963 964 973 965 965 973 974 965 975 976 965 977 977 977 978 978 978 978 978 978 978	Non Apr 19 13:23:56 1999     :   U9-08-836-455-3.zng
	Page 23		Page 21
ID V1857 standard; CDNA; 491 BP.  AC V18557,  AC V18557,  DT 05-UNN-1988 (first entry)  DE Nouse; marine; heavy chain variable region; CDNA.  KN Mouse; marine; heavy chain variable region; CDNA.  KN Mouse; marine; heavy chain variable region;  KN monoclonal antibody 2H7; human B-cell surface antigen; ss.  Fi sty.  Fi kxy  Fi sty.  Fi	CC immune reactions. They are also useful in easaying and in vitro imaging. SQ Sequence 458 BP; 113 A; 120 C; 112 G; 113 T; Out And Charlet 17.64; Score 81. DB 1; Length 458; Best Local Similarity 98.64; Ped. No. 1.06-53; Matches 141; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Marches 141; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Mismatches 141; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Mismatches 141; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Mismatches 141; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Mismatches 141; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Mismatches 141; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Gaps 0; Mismatches 2; Indels 0; Gaps 0; Gaps 0; Gaps 0; Mismatches 2; Indels 0; Gaps 0; Gaps 0; Gaps 0; Gaps 0; Mismatches 2; Indels 0; Gaps 0	Hammaculus.  1.00ation/Qualifiers  PT 855_Peptide 1.37  PT 855_Peptide 58 gs a  PT 857_Peptide 68 gs a	Non Apr 19 13:23:56 1999 U8-08-836-455-3.rng

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Page 26

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RESULT
1 V03926 standard; cDNA; 491 BP.
AC V03926; DT 01-UN-1998 (first entry)
DE Nouse 2H7 antibody heavy chain variable region.
RW Mouse; murine; heavy chain; variable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PT least the variable regions of light or heavy chains

Example YV, Fig 21, 98pp; Exglish.

CC for the prediction of an immunoglobulin (1g) fragment capable of

CO the production of an immunoglobulin (1g) fragment capable of

CO binding an antigen. The method comprises culturing an E. coli host

that has been transformed with a nucleic acid molecule encoding the

CC III fragment, under conditions so that the 1g fragment appearance

CC encoding; (2) pecture lyace screttion signal sequence

CC encoding; (2) pecture lyace screttion signal sequence

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Best Local Similarity 98 6%; Pred No. 1.30e-53;
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vile593 tanthody heavy chain variable region cDNA;
Mose: murine; heavy chain variable region;
Mouse; murine; heavy chain; variable region;
Mouse; murine; heavy chain; variable region;
Mouse; murine; heavy chain; variable region;
Mouse)cbuilin fragment production; ig fragment production;
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            immunoglobulin
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Pred. No. 1.30e-53;
0; Mismatches 2;
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REGUIT 6
ID 170868 standard; cDNA; 491 BP.
AC 170868; standard; cDNA; 491 BP.
D7 24-8EP-1997 (first entry)
D8 2BF cohain variable sequence.
EW Antibody engineering; heavy chain; light chain; chimaeric antibody;
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pri trip 21; 98pp; English.

Con the preduction of an immunoglobulin (29) (Tragment capible of control production of an immunoglobulin (29) (Tragment capible of control production of an immunoglobulin (29) (Tragment capible of control production of an immunoglobulin (29) (Tragment capible of control produced with a noticic acid molecule encoding the strain of the method comprises culturing an E. coli host that has been transformed with a noticic acid molecule and produced control produced the conditions as obtain the 19 fragment is produced control produced produces and a separate the variable region of an 19 ff molecule; and (5) pretate lyase secretion signal sequence conditions at least the variable region of an 19 light chain, where (a) and (b) are operably linked to a bush sequence encoding at least the variable consecutive of the method is used to produce champtic fab consecutive, e.g. derived from murine monoclonal antibody 207 raised convel approach for producing antiper sugineered antibodies of desired variable region specificity and constant region convel approach for producing specificity and constant region convel approach for producing specification of desired variable region appecificity and constant region convel approach for producing specification of desired variable region appecificity and constant region convel approach for producing specification of desired variable region appecificity and constant region convel approach for producing specification of specific gene synthesis, recombinant DNA cloning and production of specific gene synthesis, recombinant DNA cloning and production of specific gene synthesis, recombinant DNA cloning and production to the erficient large seale production of human control antibodies. The invention also provides a solution to the the problem of class switching antibody molecules.
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PR 25-MAR-1990, US-501092.
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PR 26-NOV-1895, US-29390.
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bonocional antibody 2H7; human B-cell surface antigen; ss.
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"JH1 sequence element"

passive immunisation; diagnosis; hybridoma; monoclónal antibody; 197; B-cell antigen; Bp35; as. Kav sp. US-08-836-455-3.rng

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RESULT 8

ID 751042; standard: cDNA; 520 BP.

AC 751042; otandard: cDNA; 520 BP.

AC 751042; otandard: cDNA; 520 BP.

DY 66-AUG-1997 (first entry)

DE Coding sequence for heavy chain variable region of 2H7.

RW Pectate lyaes; signal sequence; oran-negative bacterium; immunoglobulin;

RW protein production; human; constant region; passive immunsation; toxin;

RW antibody: Igh heavy-chain; hepatitis; mouse; lung carcinoma; cancer;

RW myeloma cell; B-cell antigen; sa

RW myeloma cell; B-ce
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PR 08-DDC-1992 US-507525.

PR 08-DDC-1992 US-5075724.

PR 08-DDC-1994 US-5075724.

PR 08-DDC-1994 US-5075724.

PR 08-DDC-1994 US-5075724.

PR 19-DDC-1994 US-5075724.

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11 13435990 A.

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18 1
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13338 ctandard; cDNA; 518 BP.
13338 correspondence of the control 
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     158
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tgcactgggtaaagcagacacct
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1 Similarity 98.6%;
141; Conservative
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71...127
/*tag= a
128..490
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 81; DB 30; Le
Pred. No. 1.30e-53;
0; Mismatches 2;
     251
180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 G; 113 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-836-455-3.rng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 520;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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NO.

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19 13:23:56

Query Match Best Local S Matches 14

17.6%; al Similarity 98.6%; 141; Conservative

Score 81; DB 31; Length 491; Pred. No. 1.30e-53; 0; Mismatches 2; Indels 0;

Gaps

109 taactacaggtgtccactcccaggcttatctacagcagtctgggggctgagctggtgaggc

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canactiption unit, provided that the 1g fragment can hind an antigen and is produced and secreted by an E. Oil host cell. when the nucleic acid molecule is expressed in the host cell. The polymuclacule molecule is used for the production of recombinant antibodies, which can be used for passive immunisation without negative immune reactions (e.g. serum sickness and anaphylactic shock), in labelled forms as immunosassy or insging response, in complement modalated lysis and for therapsuic singing proposes when completed to a toxin or other therapsuic agent.

RESULT I RESULT AC 111 
Location/Qualifiers
71.490
/\*tag= a
/product= heavy chai
/note= "no stop codo

chain variable region codon given"

e,

US5576195-A.
19-NOV-1996.
01-NOV-1985.
01-NOV-1985.
27-OCT-1986.
24-JUL-1987.
11-JAN-1988.

: 793980. : US-793980. : WO-U02269. : US-077528. : US-142039.

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Query Match
Best Local Similarity 98.6%;
Matches 141; Conservative

Score 81; DB 32; Length 518; Pred. No. 1.30e+53; 0; Mismatches 2; Indels 0;

Gaps

**₹** ₽ Ş Ş

tgcactgggtaaagcagacct

250 180

228

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US-08-836-455-3.rng

Page 33

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Query Match 16.5%; Best Local Similarity 100.0%; Matches 76; Conservative

Score 76: DB 25: Le Pred. No. 4.89e-49; 0; Mismatches 0;

Length 458

Indels

0

Gaps

US-08-836-455-3.zng

Page 34

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423 cccacccgtctatcca 438

and

DSP.2 sequence

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PR No9622373-A2.

**Transl_excpt* Pos:373..375, aa:Trp
PN No9622373-A2.

**Transl_excpt* Pos:373..375, aa:Trp
PN 15-UNI.1395; UG05372676

PR 15-UNI.1395; UG05372676

PR 15-UNI.1395; UG05372676

PR 15-ENDS; WG05372676

PR 15-ENDS; WG05372676

PR 15-ENDS; WG0527071

PR 15-ENDS
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DE TIJI33 standard; cDNA; 458 BP.

C TIJI33; (C TIJI33); (Z TIJI33);
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1..456
/*tag= a
/*transl_excpt= pos:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pos:373..375,
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RESULT 10

DE DIVIOR : tendand: cDNA: 459 BP.

AC 97-097-1991 (first entry)
DE 287 YH sequence which contains JH1 sequences and cheering antibody: settlement of the contains JH1 sequences and DE clements antibody: antibody: settlement of the contains JH1 sequences and DE clements antibody: settlement of the contains JH1 sequences and DE clements of the contains JH2 sequences and DE clements JH2 sequences and JH2 sequences and DE clements JH2 sequences and JH2 sequences and DE clements JH2 sequences and DE cleme

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PR (1702-)186; U02358.

PR (1702-)187 (EMETIC 980 INC.

PA (1802-)187 (EMETIC 980 INC.

PA (18
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                             8 8 8
                                                           Query Match 16.1%;
Best Local Similarity 98.5%;
Matches 134; Conservative
144 ctcastgasgatgtcctgcasggtttttgggtacasttaccagttacastatgcactg 203
                                       84 aggstccactccaggsttststacagcatttgggctgactgggagcctgggc 143
                                                            Score 74: DB 2: Length 459: Pred. No. 3.24e-47; 0; Mismatches 2: Indels
                                                             0
                                                            Caps
                                                             0
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19 13:23:56

1999

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US-08-836-455-3.rng
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PR 27-MAY-1955; US-447610.

PR 1070F-) ORIVERENSON TROMAS.

A DUTE-) ORIVERENSON TROMAS.

PR 1070F-) ORIVERENSON TROMAS.

PR 1070F-) ORIVERENSON TROMAS.

PR 1071 STATEMENT AND THE TROMAS THE T
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8 3 8
852 totatcc
||||||||
434 TCTATCC
                         th 14.5%; Score 67; DB 30; Length 861; Similarity 100.0%; Pred. No. 7.02e-41; 67; Conservative 0; Mismatches 0; Indels
 858
                                                  0
                          851
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Query Match Best Local S Matches 6

Length 861;

Gaps

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PER MESCLI

5 71547 etandard; CDNA; 861 BP.
7 71547, T. 1547 etandard; CDNA; 861 BP.
7 109-NG-1997 (first entry)
8 Single-therapy, antibody; encoding cD
8 Single-therapy, antibody; immuniantion; human im
8 HIV: human T-cell leukeenia virus; ss.
8 Mos mucculus;
8 Mos mucculus;
9 NOV-1996; 007393. ''i
7 23-MAY-1996; 007393. ''ii

:

REGULT 12

10 031500 standard; cDNA; 861 BP.

11 031500 standard; cDNA; 861 BP.

12 03-800.1995 (first entry)

13 10-N00.1995 (first entry)

14 11V-1. human (sequence the standard translation) gene thesapy; single chain entibody; for the standard translation; gene thesapy; single chain entibody; for a stranslation; seal first entry; first en 7

36

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Apr 19 13:23:56 1999
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US-08-836-455-3.rng

Page 37

Mon

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19 13:23:56 1999

US-08-836-455-3.rng

Page

38

pr dequence and single-chain antibody sequence has resistance to e.g. pr disrupting temperature presence of the converse control of the present sequence is the cold for the present sequence is the cold for the manusoplobulin (Is) heavy contain variable region of a murin anti-asparations II monotonal recombinant chimeric polypeptide, comprising a lat region comprising a biologically active domain and another domain of a movel comprising a single contain variable region (CC contains of a single contain antibody (ScA) having the light and heavy children as single contain antibody (ScA) having the light and heavy captions in the litter of the containing a single contain antibody (ScA) having the light and heavy captions in the litter of the containing containing the solution of the litter of the containing as a single contains and protects the sological activity from the containing agents or alcohol. The regions of the chimeric containing agents or alcohol. The regions of the chimeric containing agents or alcohol. The regions of the chimeric containing agents or alcohol the containing to contain the containing agents or alcohol the regions of the chimeric containing agents or alcohol the regions of the chimeric containing agents or alcohol the regions of the chimeric containing agents or alcohol the regions of the chimeric containing agents or alcohol the regions of the chimeric containing the solution of the chimeric containing the solution and protein of the above type has better tryps has received analogous to a sequence of the chimeric containing the solution and the chimeric containing the solution and containing the solution

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SCCCCC SALLES SALS

PN #69503832-A.

PD 09-FEED-1934.

PP 28-THIL-1934. UPG448.

PR 10-UTL-1934 UPG-098870

PR (VUZP-) UNIV\_ZEFFEESON THOMAS.

PI Duan L. Pomerant E.

PI Duan L. Pomerant E.

PI WPI: 95-092039/11.

PT sense encoding antibody binding antisen associated with a disease;

PT sense encoding antibody binding antisen associated with a disease;

PT sexuple 4: Page 23: 62pp; Ebglish.

CC Consisting of the variable domains of the heavy and light chains of a mouse Mab spaints HV-1 IIID rev. The serv psecifically conserved Rev domains. Held 74 cells expressing the Servence resistant to all HV-1 clinical isolates tested.

Sequence 861 BP: 199 A: 234 C; 230 G; 199 T;

Query Match 14.5%; Best Local Similarity 100.0%; Matches 67; Conservative Score 67; DB 14; Le Pred. No. 7.02e-41; 0; Mismatches 0;

Length 861;

Indels 0;

Gaps

0

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129 328 Query Match Best Local 6 Matches 5

h 12.8%; Similarity 100.0%; 59; Conservative

Score 59; DB 37; Length 360; Pred. No. 9.92e-34; O; Mismatches O; Indels O;

8 B

792

δ B standard; CDNA: 360

RESULT RESULT ACCORDED TO THE 
8

Of 1983-39 (first entry)
D7 OB-ARR-1998 (first entry)
D8 ARR-1998 (first entry)
D8 Immunojobulin; 19, heavy chain; variable region; murine;
EW Immunojobulin; EW Immunojohal Antibody; MAb;
EW Immunojobulin; EW Immunojobulin; EW Immunojobulin;
EW Immunojobulin; EW Immunojobulin;
EW IMMUNojobulin; EW Immunojobulin;
EW IMMUNojobulin; EW Immunojobulin;
EW IMMUNojobulin; EW Immunojobulin;
EW IMMUNojobulin; EW Immunojobulin;
EW IMMUNojobulin; EW Immunojobulin;
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Query Match Best Local s Matches 5 n 12.8%; Similarity 100.0%; 59; Conservative Pred. re 59; DB 1. No. 9.92 Mismatche DB 17; Len 9.92e-34; matches 0; Indels 0 Caps

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on DNA.
memoclonal antibody 31.6;
a; diabetes tumour;
e: rheumatoid arthritis;
st disease: nephritis;
iial ischaemis;
itherapy; ds.

RESULT:

13 74760 standard; DNA: 470 BP.

27 109-1287.197 (first entry)
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KW Alpha'4 integrin; humanised antibody; monoclonal of the standard in the standard of the standard of the standard of the standard in the standard of the standard in the standard y topy 1882 a. 1. /\*tag" b
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d \*complementarity region determining

entry)
721.6 heavy chain variable region.
1 cukocyte adhesion molecule; VLA-4;

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ID 099893; standard: CDNA; 470: 
AC 099893; standard: 

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397 tgactatggggtcaaggaacttagtcactcagtctcctcagcaaacgacaccccca
391 tgactatggggtcaaggaacctcgctaccgctctcacccaaacgaaacgaccccca

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SUPPLY AND THE PROPERTY OF THE
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11:

PD 23-UNN-1993, 121630.

PR 15-DCC-1991; DE-14307.

PR 15-DCC-1992; DE-14307.

PR 15-DCC-1
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043385 standard; cDNA to mRNA; 580 BP.

040385, 193 (first entry)
2 46-027-193 (first entry)
3 46-027-193 (first entry)
4 Nochalo 1-region of monoclomal antibody A2AA1.
4 Nochalo 1-region of monoclomal antibody A2AA1.
5 101 1917: 18; heavy; 29; immunoglobody 15; V; va
5 101 1917: 18; heavy; 29; immunoglobody A2AA1.
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T70805 standard; DNA; 477 BP.
T70805;
10-JUL-1997 (first entry)
Nouse anti-idotypic anti-BOFR; epidermal growth factor receptor; tumour: cancer; neoplasia; glione; melanoma; carcinoma; drug manufacture; sakus musculus.
Location/Qualifiers
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cds
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L4470
League post55.57, as: L/
Lague post55 cdon given*
L527
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L152
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/*tag= a
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Query Match Best Local Similarity

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No. 59:

DB 7; Length 588 9.92e-34;

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Procedures comprising lyophilised compan conts, Deskins fibrin prescipers, buffer and subhilising open; for we insubble fibrin prescipers used for evaluating pre-disposition to thrombotic event BB Disclosure; Page 97: 10pp; English.

Con The present sequence snodes the MHI monoclonal antibody heavy contents on the meaning of the content of the conte
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19-DEC-1996 U07891.

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07-UNH-1995 US-468420.

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T59339;
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21-AUG-1997 (f
EMH: monoclonal
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germfree animal
Hus musculus.
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antibody heavy chain encoding cDNA.
in: antigen binding site: antigen free animal;
i: immunoreactive: thrombotic event; ss.
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/label* encodes_CDR1
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8 B OSISSI standard; DNA; 1147 BP.
OSISSI standard; DNA; 1147 BP.
OSISSI standard; DNA; 1147 BP.
121-MAY-1994 (first entry)
Sequence encoding mouse anti-bovine growth hormone MAb heavy chain.
Monoclonal antibody; MAB; affinity; binding; antigen; diagnostics;
Merappy; Langing; purification; biosensors; ss.

Key mseculus.

Location/Qualifiers

Misc\_difference 7.08 pp. 100 pp. 1 misc\_difference misc\_difference misc\_difference 371 504 /\*tapa a /rtanal\_except= (
201.303
/\*tapa /rtanal\_except= /rta Š G Š AGT encodes encodes Serine Glutamine

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polypeptide can be used in diagnostics, therapy (in vivo and in vitro), imaging, purifications and biosensors sequence 1347 BP; 341 A; 383 C; 333 G; 290 T; Length\_1347;

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Query Match Best Local S Matches 5 h 12.8%; Score 59; DB 9; Len-Similarity 100.0%; Pred. No. 9.92e-34; 59; Conservative 0; Mismatches 0; Indels 0; Gaps

0

390 429

δ **β** 

RESULT 20
ID 729056 atandard: cDNA; 1347 BP.
AC 729056; 200 Clirat entry)
DT 13-NOV-1996 (first entry)
DE Murine anti-BGH MAD heavy chain cDNA.
RW Antibody engineering; monoclonal antibody; MAI
RW Alighe chain antibody; immunoassay; bovine grc
RW Mis muscullis.
Location/Oun'! \*\* /\*tag= a /transl\_except= ( 640..642 /\*tag= b /transl\_except= ( (7..9, aa:Gln) MAD; heavy chain; growth hormone; BGH;

(640.

.642, aa:Ser)

DE 21 MAXI-293.

PR 21 MAXI-293.

PR 22 SEP-1936. US-0271.

PR 02 SEP-1936. US-0271.

PR 02 SEP-1936. US-0271.

PR 02 SEP-1936. US-0271.

PR 02 SEP-1936. US-0271.

PR 03 SEP-1945. US-0271.

PR 05 SEP-1945. US-0271.

PR 19-1MN-1995. US-0917.

PR 19-1MN-1995. US-0917.

PR 19-1MN-1995. US-061988.

PR 1820-1 ERZON LABS INC.

PR 06-7UN-1995. US-061988.

PA (ERZO-) ERZON LABS INC.

PA 19-1MN-1995. US-06198.

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Til733 standard: cDNN: 1347 BP.
Til733 standard: cDNN: 1347 BP.
Til733 standard: cDNN: anci-Dody heavy chain cDNN.
Anti-Dod monoclonal anci-Dody heavy chain: light chain monoclonal anti-Dody subbeavy Chain: light chain: monoclonal anti-Dody subbeavy Chain: Location/Qualifiers
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Cds 7..9

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PR 03534621A.

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PR 03505-1896.

PR 02-SEP-1896.

PR 02-SEP-1896.

PR 02-SEP-1897.

PR 02-SEP-1897.

PR 03-SEP-1897.

PR 05-MRR-1899.

PR 05-WR-1899.

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PR 05-WR-1899.

PR 06-WR-1895.

PR 06-WR-1

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Query Match 12.8%; Best Local Similarity 100.0%; Matches 59; Conservative Score 59; DB 22; Le Pred. No. 9.92e-34; 0; Mismatches 0;

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standard; DNA; 1528 irst entry)
amma anti-carcinoembryonic
as mRNA; carcinoembryonic
Location/Qualifiers
30..1430 8

RESULT 23

ID M4005; Standard: DNA;
AC M4005; Other search
DT 01-DDC-1991 (first se
DE M8NA encoding gamma at
KW Immunopiobulin: se mRI
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10-1891 (1991 (1991)
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1 12.8%; Similarity 84.7%; 50; Conservative Score 59; DB 3; Len Pred. No. 9.92e-34; 9; Mismatches 0; Indels 0; Gaps 473 429

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RESULT 24 ID N40024

Page 47

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Page 46

molecules (W02188-90) the characteristics of the a chains of the variable x Sequence 1347 BP; ) that, upon the aggregate le region of 341 A; n refolding, have the of the 2 original f the antibody.
383 C; 333 G; the binding al heavy and

Query Match Best Local S: Matches 5: h 12.8%; Similarity 100.0%; 59; Conservative Score 59; DB 23; Length 1347; Pred. No. 9.92e-34; 0: Mismatches 0; Indels 0; 290 T; Gaps

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RESULT 21
10 (007708 standard: DNA; 1347 BP.
10 (007708 standard: DNA; 1347 BP.
11 (007708 standard: DNA; 1347 BP.
12 (007708 standard: DNA; 1347 BP.
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14 (007708 standard: DNA; 1347 BP.
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16 (007708 standard: DNA; 1347 BP.
17 (007708 standard: DNA; 1347 BP.
18 (007708 standard: DNA; 1347 BP.
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D 0/9990; standard; CDNA to mRNA; 1553 BP.
C 0/9990;
T 01-SEP-1995 (first entry)
E Anti-tobacco measic virus monoclonal Ab heavy chain cDH
W Tobacco measic virus iTV; monoclonal antibody;
W heavy chain; virus-resistant plants; biofarming; es.
Synthetic.
Location/Qualifiers
T cds
55:1453
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08-ARR-1998 (first entry)
Chimeric gene containing anti-asparaginase MAb light
Immunoglobulin, 1g; heavy chain; variable region; mur
asparaginase II; monoclonal antibody; MAb; light chair
recombinant chimeric polypeptide; as.
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346 standard; cDNA; 1848 BP.
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Pred. No. 9.92e-34;
0; Mismatches 0;
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RESULT 28

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pp 07-MX-1993; 111208.

pp (07-MX-1993; 1)-111208.

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20-JUN-1994: UB-9874.
28-JUN-1994: UB-9874.
(CEBA ) CEBA DEZICY AG.
CATOZIA JOHN ACEICY AG.
WPI: 96-07944/08.
New momoclonal antibodies which bind insect gu
partic. with toxin moleties for the control of
in planes
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Claim 8; Page 68-72; 106pp; English.
T15725-35 are DNA mols. encoding a monoclonal
fragment. MAbs were produced by using insect ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JWH-1996 (first entry)
381 single chain antibody DNA from pc:E4631.
481 single chain antibody DNA from pc:E4631.
48280; malie; pesticide; brush border membrane vesicle; monoclonal;
48280; malie; pesticide; brush border membrane vesicle; monoclonal;
48280(0781-A).
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1371 TagacThcTagacThAnacaAnccTcAgTcAccGTCTCCTCAGCCANANCAANACCCCA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          675 tggactactggggtaanggaacctagtcaccgtctcctcagccaaangaaacccacca 733
371 TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCAGCAAAACGACACCCCCA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 12.8%; Score 59; DB 37; Length 1849
Similarity 100.0%; Pred. No. 9.92e+34;
59; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 12.8%;
Similarity 100.0%;
59; Conservative
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Pred. No. 9.92e-34;
O; Mismatches O; Indels
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activated
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US-08-836-455-3.zng

Page 53

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US-08-836-455-3.rng

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                                Query Match 12.8%; Score 59; DB 1; Len Best Local Similarity 100.0%; Pred. No. 9.92e-34; Matches 59; Conservative 0; Mismatches 0;
                                                                 produced.
see also Q04654.
Sequence 3343 BP;
815 A;
                                                                 871 C;
                                                                846 G;
                                                Length_3343;
                                                                811
                                Indels
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JC2-25 etandard; DNA; 402 BP.

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signal\_peptide

Location/Qualifiers
1..402
/\*tag= a
/\*tog= anti-idiotype\_antibody\_Idio17
1..30
/\*tag= b

18 ANR-1955.

18 ANR-1955.

18 ANR-1955.

19 ANR-1955.

19 Corr-1951 272550.

29 Ge-Corr-1951 272550.

29 Ge-Corr-1951 272550.

20 Ge-Corr-1951 272550.

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21 Ge-Corr-1951 272550.

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23 Ge-Corr-1951 272550.

24 Ge-Corr-1951 272550.

25 Ge-Corr-1951 272550.

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27 Ge-Corr-1951 27250.

28 Ge-Corr-1951 27250.

29 Ge-Corr-1951 27250.

20 Ge-Corr-19

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Query Match 12.4%; Score $7, DB 16; Length 399; Best Local Similarity 100,0%; Pred No. 5.83-22; Length 399; Matches 57; Conservative 0; Mismatches 0; Indels 0;
399
                                               Gaps
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Noveles 1. 140 years in the control of the antibody useful in antibody. Laddy against an human anticancer monoclonal antibody. I amedita sequences encoding the antibody, useful in pharmacology medita sequences of the control of the
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Page 55
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US-08-836-455-3.rng

RESULT
ID 17
AC 17
AC 17
AC 30
DE MO
KW An
KW CA
OS Mu
FH Ke

T70808 standard: DNA: 474 BP.
DO-JUL-1997 (first entry)
DO-JUL-1997 (first entry

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Ouery Match 12.4%; Score 57; DB 16; Length 402; Best Local Similarity 100.0%; Pred. No. 5.83e-32; Matches 57; Conservative 0; Hismatches 0; Indels 0;

Gaps 402

0

346 organizatigasteaagaacoteagteacogtetocteagceaaaacgacacco

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primer_bind
         primer_bind
                                     signal_peptide
1..57
/*tag= b
1..25
/*tag= c
/*tag= d
```

primer\_bind primer\_bind signal\_peptide

/\*tag= a /transl\_except= p /mote= no stop c 1.57 /\*tag= b 1.30 /\*tag= c 448.474 /\*tag= d

pos:388..390, aa: codon given\*

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PH 29-745512-A1.

PH 2002-1996. 197551.

PH 44-DEC-1996. 197551.

PH 44-DEC-1996. 197551.

PH 44-DEC-1996. 197551.

PH 42-DEC-1996. 197551.

PH 42-DEC-1995. 22-DEC-1996.

PH 42-DEC-1995. 22-DEC-1996.

PH 42-DEC-1995. 22-DEC-1996. A., Gomes A., Piulate J., Rosell E;

PH 44-DEC-1995. 23-DEC-1996. A., Fiulate J., Rosell E;

PH 42-DEC-1995. 23-DEC-1996. A., Piulate J., Rosell E;

PH 42-DEC-1996. A., Gomes A., Piulate J., Rosell E;

PH 42-DEC-1996. A., Gomes A., Piulate J., Rosell E;

PH 42-DEC-1996. A., Gomes A., Piulate J., Rosell E;

PH 42-DEC-1996. A., Gomes A., Piulate J., Rosell E;

PH 42-DEC-1996. A., Gomes A., Piulate J., Rosell E;

PH 42-DEC-1996. A., Gomes A., Piulate J., Rosell E;

PH 42-DEC-1996. A., Gomes A., Piulate J., Rosell E;

PH 42-DEC-1996. A., Gomes A., Piulate J., Rosell E;

PH 42-DEC-1996. A., Gomes A., Piulate J., Rosell E;

PH 42-DEC-1996. A., Gomes A., Piulate J., Rosell E;

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PH 42-DEC-1996. A., Gomes A., Piulate J., Rosell E;

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PH 42-DEC-1996. A., Gomes A., Piulate J., Rosell E;

PH 42-DEC-1996. A., Gomes A., Piulate J., Rosell E;

PH 42-DEC-1996. A., Piulate J., Rosell E;

PH 42-

Query Match 12.4%; Best Local Similarity 100.0%; Matches 57; Conservative Score 57; DB 30; Length 474; Pred. No. 5.83e-32; O: Mismatches O; Indels O;

Ś 8 394 gactactgggtcanggaacttagteaccgtttccttagccaanacgacacccca 450

0

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RESULY 33
TD 714615; standard: DNA; 454 BP.
AC 714615; Man-1997 (first entry)
DE Humanised anti-CD19 monoclonal antibody variable heavy chain,
KW MONOCLONAL antibody; Mb; humanised; cancer; autolumine disease;
KW MONOCLONAL antibody; Mb; humanised; cancer; autolumine disease;
KW MONOCLONAL antibody; Mb; humanised; cancer; autolumine disease;
KW MONOCLONAL Autology; Mphoma; rheumaroid arthritis; CD39; chain; de.
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OS Mum masquas.
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Location/Qualifiers
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(https://processing.com/p

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RESULT
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AC 17
DT 30
DE MO
DE MO
RW An
RW An
RW An
RW An
RW CA

1770310 standard; DRN; 474 BP:
1770310 standard; DRN; 474 BP:
1770310;
10-JUL-1997 (first entry)
10-JUL-1997 (first entry)
10-JUL-1997 (stret entry)

Location/Qualifiers
1..474 /\*tag= a /note= "no stop codon given"

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Overy Match 21.4%; Score 57, DB 30; Length 474; Best Local Similarity 100 0%; pred. No. 588-2.7; Matches 57; Conservative 10; Mismatches 0; Indels

Length 474;

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Page 56

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cc NN-01 is a monoclonal antibody. In order to characterise the curief epitope recognized by NR-01, the antibody was screened by CIIAA for reactivity with overlapping peptides corresp, to the anino call sequence of the VI loop region of HVV-1 pp.30 (N3333, R3333), can also with the heat was no detectable reactivity over background of the VI loop region of HVV-1 pp.30 (N3343) and the CIIAA corresp, to have plotted representations of the CIIAA corresp, to have plotted representative by the secretary contained an extension of the period of the corresp to the VI loop binding per the secretary contained by the secretary with other corresp to the VI loop binding per the secretary contained by the corresp to the VI loop corresp. The corresp to the VI loop corresp to the VI loop corresp. The secretary corresp to the VI loop corresp. The variable region of the heavy and light chain of monoclonal corresp. The period sec out in R3344. Corresp. Corresp. The period corresp.
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Profisences and a recipient framework of human or primate origin, boreign origin can are activent framework of human or primate origin, where the corresponding observable of the heavy (H) chain of the framework is replaced by an amino acid the same as or similar to contain the corresponding position of the R chain of the Ab from the corresponding position of the R chain of the Ab from the corresponding position of the R chain of the Ab from the corresponding position of the R chain of the Ab from the corresponding position of the R chain of the Ab from the corresponding position of the R chain of the Ab from the corresponding position of the R chain of the Ab from the corresponding to the corresponding to the framework of the corresponding to the humanised Ab with the original domework of residues 29 and 78 of the humanised Ab with the original domework of residues are response the antispen binding activity of the antispendicular activities of the activity of the antispendicular activities and activities activities activities activities activities and activities activities and activities activities activities activities activities and activities activiti
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N91645:

EP-33895-A.

25-CCT_189; 10463.
112-PB-189; 10463.
19-PB-189; 10463.
19-PB-189; DZ-811023.
(REMY) Behringworke.
Comday H, Karget H, von Specht BU;
HPI: 89-11085/J.
P-PERB: p-3079/J.
P-PERB: p-
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28-NOV-1999; GB-02449.
02-DEC-1999; GB-02449.
(NELL) HILLOME POUND ILLIAMS, LLAVÍS AP.
EDI: 96-27772/2/8.
P-EDD: R99941.
Humanised monoclonal ant 79 - esp. against CD38,
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Pred. No. 1.42e-27;
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Pred. No. 5.71e-25;
0; Mismatches 0; Indels
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RESULT 35

RESULT 35

DE 37731 standard: DNA; 402 BP.

AD 037431.1993 (first entry)
DE 36quence exceding the variable region of the
DE monoclosal antibody NN-01; MIV-1; 9p120; 9p1
OS Synthetic. Location/Qualifices
FR Key 1.402
FT cds //tag= a
PN 409304090-A.
PP 24-NAG-1992; U07111.
PR 22-NAG-1992; U07711.
PR 22-NAG-1992; U07711.
PR 23-NAG-1992; U07711.
PR 24-NAG-1992; U07711.
PR 24-NAG-1
RESULT 3

RESULT
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Presentant or disposis of HYV-1 infection.

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Natches 49; Conservative
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1992 1993 1997 145 A5 144 CC 1310 G; 121 T;
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P-980B R31344.
P-980B R31344.
Monocional actioodes against HTV-1 gpl20 and gp160 for creating and preventing HTV-1 infection Example: Page 34-35; 57pp; English.
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371 TGACTACTGGGTTAAGGAACCTCGTGACCACTCTCTCAGCCAAAAC 419
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US-08-836-455-3.rng

690

ő Gaps 9

7 .-

Query Match 10.6%; Best Local Similarity 100.0%; Matches 49; Conservative Score 49; DB 33; Id Pred. No. 5.71e-25; 0; Mismatches 0; Length Indels

d4384) standard: DNA; 417 BP.

043843; standard: DNA; 417 BP.

04007-1993 (first entry)
Chimeric 128 1 VH, mouse gemma subgroup IIP DNA; murine; heav
nolymerase chain reaction; primer poRs, amplify; murine; heav
1191t; chain; veriable; constant; region; anti-thoman; transfer
receptor; antibody; brain; capillary; endothelial cell; conjuneuropharmaceutical; diagnostic; appait; tumour; AlDS; stroke;
ppliepy; Parkinsons disease; Alcheimers disease; sa,
annibetic.

mat\_peptide signal\_peptide Location/Qualifiers 1..57 "Leader sequence" ٣

West word of the control of the cont

Query Match Best Local Similarity 100 92 Score 47: DB 7; Length Pred. No. 3.01e-23;

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PR 05.576.194.A.

PR 05.576.194.A.

PR 05.58D-1968. 240.524.

PR 05.58D-1968. 205-240.524.

PR 05.58D-1968. 205-240.524.

PR 05.58D-1968. 205-240.524.

PR 10.58D-1968. 205-250.025.

PR 10.58D-1968. 205-240.025.

PR 10.58D-1968. 205-240.

PR 10.58D-1968. 205-240.025.

PR 10.58

Query Match Best Local Similarity 10.21; Length 480

par

TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAA 417

UUT 40
T13442: standard; cDNN; 480 BP.
T13442: 113-PEB-1997 (first entry)
NBb milo heavy chain variable region cDNA.
Chimeric antibody; monoclonal antibody; RM10; antibody engineering;
tumour; entigen; colon carcinoma; stomach carcinoma;
cesophisus carcinoma pancreas carcinoma; cancer; diagnosis;
therapy; heavy chain; ss.
therapy; heavy chain; ss.
Location/Qualifiers
64.,880 64.880

Location/Qualifiers 64..480 /\*tag= a /product= RM10 heavy c

Page

8

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Matches

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47; Conservative 0 Mismatches 0 Indels 480

0

Gaps

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CD20:

2BS. peripheral

P7000

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RESULT:

AC OSSELL standard; DNN; 420 BP.

BY 01 1983-1995; (210st cartibody; CD2

KW 8 cell lysis; as

OS Mis misculis.

PN 009411026-A.

PD 25-NA; 1994.

PP 11-NOV-1993; U0-978891.

PR 11-NOV-1993; U0-978891.

PR 11-NOV-1993; U0-140999.

PA (1DEC: ) IDEC PINKHE CORP.

PA (ADEC:) IDEC:

PA (ADEC:) IDEC: pril-Nov.1893.

pril-Nov.1893 US-978891.

pril-Nov.1993 US-97891.

pril-Nov.1993 US-97891

derived from

Query Match Best Local S Matches 4 h 10.0%; Similarity 100.0%; 46; Conservative Score 46; DB 11; Length 420 Pred. No. 2:17e-22; 0; Mismatches 0; Indels

Length 420;

Gaps

0

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RESULT 42

ID 055639 enandard: DNA: 9208 BP.
AC 055639;
DT 01-FEB-1995 (first entr)
DE Vector conty, TAXE 8 DNA.
KW 8 cell lymbhoma chimeric antibody; CD20;
GS Synthetic. peripheral blood

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MOD

Matches

47;

371

Page 62

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Conservative 0 Mismatches 0 Indels 0 Gaps

0

RESULT 39

OBSID standard; DNA; 480 BP.

O OBSID standard; DNA; 480 BP.

O OBSID standard; DNA; 480 BP.

DY OH-NAS-1993 (first entry)

DE NAIO BROAY Chain Y Region (souse).

RM Monoclosery chain Y Region (souse).

RM Monoclosery chains ; Light; heavy; chain; constant;

RM warship annihopy; chimeta; Light; heavy; chain; constant;

RM warship annihopy; chimeta; Light; heavy; chain; constant;

RM Warship annihops; chimeta; chimet tggactactggggtcaaggaacctcagtcaccgtctcctcagccaaa 417

Location/Qualifiers 64..480 /\*tag= a

RESULT AND DATE OF STATE OF ST RR, Lei S, Chang

Chimeric mouse-human antibodies - prepd. using constant human region murine variable region, antigen genes coding for esp. to 3 tumour

antigm:
Claim 13: Page 133 + Pig 36: 173pp; English.
Claim 13: Page 133 + Pig 36: 173pp; English.
Claim 14: the nuclectidate statement from the end of the oligo-dC tail to the Jhi-full junction expense from the used in the product of a chineric antibody mol. comprising two lasts and two heavy chains, and constant region (human) and colaims and unrine) having specificity to an antigen bound by muricabone region (murica) (Mab) Rúlo. The oligent antibods which the original murica subsect and by muricabone region (murica) which the original murica subsect has the diagnosis and treatment of cancer.

They are more compatible with the human body. They are esp. used for the diagnosis and treatment of cancer.

Sequence 400 pp; 130 A; 133 C; 127 G; 110 T;

434 tygactactygygtcaaggaacctcagtcaccgtctcctcagccaaa h 10.2%; Similarity 100.0%; 47; Conservative Score 47; DB 5; Length 480; Pred. No. 3.01e-23; O; Mismatches O; Indels . Caps

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US-08-836-455-3.rng

Page 65

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Page

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RESULT 45

ID 056685 standard: DNA: 402 B:

ID 056685 standard: DNA: 402 B:

DT 03-SEP-1994 (first entry) b

IV 03-SEP-1994 (first encoclonal intibody NN-01 heavy chain because the concoclonal intibody NN-01; variable and spirope; monoclonal intibody NN-01; variable b Synthetic.

EN Synthetic Location/Qualifiers

EN Key 11-402
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ACT
DT 25
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PI Reffine;
PI Reffine;
RHP1; 94-183162/22.
RHP1; 94-183162/22.
PI Treating B cell lymphoma with chimeric antibody - against CD20,
PI Treating B cell lymphoma with chimeric antibody - against CD20,
PI Treating B cell lymphoma by the chimeric antibody and proposed and hybridomas Buglish.
PI antibodies and hybridomas Buglish.
PI antibodies and hybridomas English.
PRAES, agne sascoding a chimeric content proposed and proposed anticequenctions a vertex conteg. Buglish.
PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PRAES, PR
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Best Local S
Matches 4
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Best Local Similarity 100.0%;
Matches 46; Conservative
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W09600783-a
11-JAN-1996
20-JUN-1995
28-JUN-1996
(CIBA) CIE
CAFOZZÍ NB.
WPI; 96-077
P-PSDB; R90
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26-MAY-1994;
12-N0V-1993;
13-N0V-1993;
(IDEC-) IDEC I
Anderson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2497 ctggggottagtgaagatgtottgcaaggttottggotacacatt 2542
98 ctagacctetarahaartetoorahaacttottoorahaactt
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15727;
15727;
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5-JUN-
95 hea
11ta e
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reavy chain wartable region DNA from pCTB4615.
endotoxin: Beallius thuringtensis; western corn rootworm;
maise; pesticide; brush border membrane vesicle; monocional;
cory; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0783-A1
N-1995, IB0497,
N-1994, US-267641.
) CIBA GELGY AG.
DE MS FORIET AG.
E: MS FORIET AG.
96-077494/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.5%; Score 44: DB 5; Length 360; Similarity 100.0%; Pred. No. 1.09e-20; 44: Conservative ; 0; Mismatches 0: Indels
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; U5-978891
; U5-149099
; C PHARM CORP
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Location/Qualifiers
1..402
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/label* hFR3
301.327
/*tag* f
/label* hCDR3
328.361
/*tag* g
/label* hFR4
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                                                                                                                                                               AIDS: glycoprotein; V3
NM-01; variable heavy;
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(MISP) NESSH SHOWNAM KAISHA LTD.

(MISP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.5%;
Best Local Similarity 100.0%;
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 13:23:56
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PT New monoclonal antibodies which bind insect gut proteins - used practic. With toxin moleties for the control of insect peaks, partic. Part in plants of the control of insect peaks, partic. Part in plants of the plants of the partic peaks of th
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Best Local Similarity 100.0%;
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 18; Length 372
Pred. No. 1.55e-21;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPS;
11 58-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
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-1993; U07967.
-1992; WO-U07111.
-1993; US-039457.
) MISSIN SHOKUHIN KAISHA
                                                                                   /*tag*
                                                                                                                                     US-08-836-455-3
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Page

Score 44; DB 10; Length 407 Pred. No. 1.09e-20; 0; Mismatches 0; Indels Length 402;

6

Gaps 0

RESULT 46

ID 028746 standard; DNA; 417 BP.

ID 028746; 038746; 038746; 04874 chirp; por 01.4Mar.1999 (first entry)

EX Anti-CEA specific heavy chain variable region DN

REAL CONTROL OF THE PROPERTY OF THE i DNA. .: light chain; ' ring; es.

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rage

mat\_peptide

/\*tag= 58..417 /\*tag=

**p** 0

mat\_peptide

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PH J04214987-A. /\*Tag\* D
PH J04214987-A. /\*Tag

Query Match 9.5%; Best Local Similarity 100.0%; Matches 44; Conservative Score 44: DB 5: Length 417: Pred. No. 1.09e-20; 0: Mismatches 0: Indels

> 0 Caps

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SULY 48
SULY 48
T04632 standard; DNA; 336 BI
T04632:
T04632:
33-RAY-1996 (first entry)
House derived heavy chain R
Heavy chain; RT3; murine; ca

RT3 phage catalytic 무

antibody;

Query Match 9.5%; Best Local Similarity 100.0%; Matches 44; Conservative

Score 44; DB 6; Length 417; Pred. No. 1.09e-20; O; Mismatches 0; Indels

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8 B

Cancer. (first entry)
Lo mouse heavy chain
Libody: human cancer DNA: 417 chain region. antigen; treatment

IRESULT
AC TOO
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Location/Qualifiers
1..336
/\*tag= a
/note= "partial peptide"

pattern D; ss. Mus musculus. Rey cds

WOS27045-Al.
12-027-1995
30-MAR-1994; U03420
30-MAR-1994; WO-003420
(ICEN-) ICEN INC.
CLIEBELL D. DEFREY MJ. Fitsgerald K. Kenten
Martin MT. McCafferty J. Smith RG, Titmas RC.

JE; Williams

Location/Qualifiers
1.417
/\*tag= a
/note= encodes heav;
40.42
/\*tag= b
/note= should encode should encode encodes heavy

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should read TTA?"

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REFFERNSSSS war. 95.35864/46.

P-BEDR REGORS.

P-BEDR REGORS of establytic antibodies displayed on phage - by generating of establytic antibody-derived domains and expressing generating a gene library of antibody-derived domains and expressing the phage vectors 1312pp; English the presence of the producting the DNA was used in the preph. of catalytic antibody (CA) producing the DNA was used in the preph. of catalytic antibody (CA) producing bacteriophage. The CNA can be used to activate descript the body of the DNA was used in an adiable by enhancing the rate of cleavage, or formation of a specific bond within a mol. in vivo.

Sequence 336 BP; 89 A; 86 C; 84 G; 77 T;

Query Match 9.3%; Best Local Similarity 100.0%; Matches 43; Conservative Score 43; DB 17; Le Pred. No. 7.69e-20; 0; Mismatches 0; Length 336; Indels 0

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19 standard: DNA; 348 BP.
188139 standard: DNA; 348 BP.
18818198 (first entry)
Variable heavy chain of MAb Lt2 DNA;
Variable heavy chain; B cell; monocional antibody; Mab; Lt2;
Variable heavy chain; B cell; monocional antibody; Mab; Lt2;
B cell tymphoma: lymphocytic leukaemia cell; murine;
diagnosis; trastment; B cell malignancy; non-Hodgkins lymphoma;
chronic lymphocytic leukaemia; da,

mat\_peptide Location/Qualifiers 1..348 , /\*tag= a

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specific anti-B cell lymphoma and anti-lymphocytic lenkemia cell mutine MAb. In the Mab can be used to disgnose or treat B cell malignancies, e.g. non-Bodykins lymphoma or chicolic lymphocytic lenkemia. The glycosylation site allows a label or therapeutic agent of increased site to be conjugated to the carbohydrate mostery, without affecting the MAb's binding affinity oer specificity.

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GenBank, Release 110.0, Released on 14Dec1998, Formatted on 15Dec1998

EMBL, Release 56.0, Released on 16Sep1998, Formatted on 15Dec1998

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applicant: foon, kenneth a.
applicant: chatterjee, sunil k.
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7) Sequence 3 from patent US 57
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REYNORDS Unknown.

SOURCE DAKNOWN.

ORGANISM Unknown.

REFERENCE 1 (based 1 to 458).

AUTHOR'S Robinson, R., Liu, A.Y., Hellstrom, K.E., Hellstrom, I. and Ledbetter, J.A.

PATE THE DOLLARS ALL SPECIFICITY TO human B cell surface antigen JOHNAL Baten: EP 0774384 AL 37 13-UL-1888;

FENTURES 1-488 1-488 1-488.
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ORGANISM synthetic construct.

ORGANISM synthetic construct.

REFERENCE 1. Loads 1. sequence.

AUTHORS Chen Z. C. Cockburn M., Torrance, L., Barker, H. and Whitelam, G.C.

TITLE Cytoplessic accumulation of a soluble functional scry protein to a

plant virus expressed as a thioredoxin fusion in Escherichia coli

REFERENCE 2. (Dames 1 to 902)

AUTHORS Chen, E.C., Cockburn, M., Torrance, L., Barker, H. and Whitelam, G.C.

AUTHORS Chen, E.C., Cockburn, M., Torrance, L., Barker, H. and Whitelam, G.C.
                                                                                                              KEYWORDS
SOURCE
                                                                                                                                   RESULT 4 10011 450 bp DEFINITION Sequence 12 from Patent WO 8804936. ACCESSION 108811 10881 9586489
SOURCE Unknown.
ORGANISM Unknown.
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1 (bases 1 to 458)
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Oy 77 CTGGGCTGAACTGCTGAGGCTGGGCCTCACTGAAGATGTCTGCT 136
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LOCUS 105921 458 bp
DEFINITION Sequence 37 from Patent EP 0274394.
LOCESSION 105921
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Best Local Schilarity 92.3% Pred No. 2.88e-78;
Matches 127; Conservative 0; Minatches 1; Indels 0; Gaps 0;
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137 ACACATTACCAGTRANATACCACTGGGTANACGAGACCTGGAACGGCCTGGAAT 196
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Submitted (23-2729-1998) 2 C. Chen, Botany, Univ. of Leicester,
University Read, Leicester LEI 7RH, UK
L. 1002
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136 CTGGGGCCTCAGTAAGATGTCCTCCAAGGCTTCTGGCTACACATTTACCAGTTACAATA 195
98 CTGGGGCCTCAACTACAATCACCTCTCCAGGCTTCTGCTTAGAATTACAAGTTACAATTACAAGTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTAC
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COVRG 279 bp RNA ROD 13-OCT-1993 Sculus immunoglobulin gamma heavy chain (DBA/1) gene, v region.

Eukaryotae: mitochondrial eukaryotes: Metazoa: Chordata; Vertebrata: Eutheria: Rodentia: Sciurognathi: Myomorpha: Muridae;

(bases 1 to 279)
Al., Bona,C.A. and Holmdahl,R.
riable region gene selection of immunoglobulin G expressing B
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FEATURES
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Robinson,R.R., Liu,A.Y., Hellstrom,K.E., Hellstrom,I. and Ledbetter, 100,4936-A 12 14-JUL-1988; Eccation/Qualifiers
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INCUSTOR S 109199 458 bp DEFINITION Sequence 30 from Patent WO 8900999. MCCESSION 109199 NID \_\_ 9588126 PAT 14-NOV-1994

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JOURNAL FEATURES Source REFERENCE AUTHORS TITLE BASE COUNT ORIGIN SOURCE Unknown
ORGANISM Unknown Patent: WO 8900999-A 38 09-FEB-1989; Location/Qualifiers 1. .458 Unclassified.

( beset 1 to 458)

Robinson,R.R., Liu,A.Y., Horvite,A.H., Wall,R.
MODULAR ASSEMBLY OF ANTIBODY GENES, ANTIBODIES /organism="unknown"
113 a 120 c 112 g 113 t and Better, M.
PREPARED THEREBY AND

JOURNAL MEDLINE FEATURES SOURCE

94009207

Location/Qualifiers
1. .279

REFERENCE AUTHORS TITLE

rect Submission
matted (02-AGC-1993) John A Mo, Department of Medical and
ysiological, Department of, Medical and Physiological Chemistry,
sargatan 3, Uppsala, 75123, Sweden
(Dases 1 to 279)
(Dases 1 to 279)
(A. Bona,C.A. and Hondahl, R.
VIJA., Bona,C.A. and Hondahl, R.
Uriable region gene selection of immunoglobulin G-expressing B
plls with specificity for a defined epitope on type II collagen
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Ouery Match 27.6%; Score 81: DB 22; Length 458; Best Local Similarity 98.6%; Pred No. 9.39s-61; Matches 141; Conservative 0; Himmatches 2; Indels 0; Gaps

76 TAACTACAGGIGICCACICCCAGGCITAICTACAGCAGICIGGGGCIGAGCIGGIGAGGC 135

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CDS gene

76 a

BASE COUNT ORIGIN

Query Match 16.5%; Best Local Similarity 99.1%; Matches 106; Conservative 20 CTGGGGCCTRAGRAMGATGTCCTRCAMGGCTTCTGGCTRACACATTTACCACTTTACAATA 79 CTGGGGCCTCAGTGAMGATGTCCTRCAMAGGCTTCTGGCTRACACATTGACCAGTTACAATA 157 Score 76; DB 29; Length 279; Pred. No. 2.36e-55; 0; Mismatches 1; Indels 0; Gaps

JOURNAL REFERENCE AUTHORS TITLE JOURNAL Vertenacu.

I (bases 1 to 292).

Ko.J.N. Bona.C.A. and Holmdahl.R.

No.J.N. Bona.C.A. and election of immunoglobulin G expressing B callable properties of the service of t

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V\_region

Organism="the musculus"

\*\*tain="phA."

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/fissus-type="lymph node"

/cail\_type="go cail hybridona"

/cail\_type="lgo cail hybridona"

/cail\_tine="Circis40 hybridona"

/chtomasome="lgo"

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JOURNAL MEDLINE FEATURES SOUICE cells with specificity for a defined epitope on type II collagen Bur. J. Immunol. 33 (10), 2503-2510 (1993) 94009207 Location/Qualifiers

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SGS

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Query Match 16.5%; Best Local Similarity 99.1%; Matches 106; Conservative 20 CTGGGGCCTRAGTAMAINTECTRCAMAGCTTCTGGCTMARATTTMCCAGTTMANTA 79
98 CTGGGGCCTRAGTAMAINTECTRCTMCCMCCTTCTGGCTMCACATTTMCCAGTTCACATTACAATT 157 Score 76; DB 29; Length 282; Pred. No. 2.36e-55; 0; Mismatches 1; Indels 0; Gaps

RESULT 8

DEFINITION I Museculus immunoglobulin gamma heavy chain (DBA/1) gene, v region ACCESION 25445

REPARDED HAM PROBLEM MHIGGCVRC 285 bp. RUA. ROD 13-0CT-1993 K.muscrius immunogiobulin gamma heavy chain (DBA/1) gene, v region. Z2348

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Cocation/Qualifiers

US-08-836-455-3.rge

No.7.A., Bona.C.A. and Holadahl, R.
Variable region gene selection of immunoglobulin G expressing B
cells with appeniately for a defined epitope on type II collagen
Eur. J. Immunol (1993) In press
2 (bases 1 to 285)

Page 30

Direct Submission
Submitted (02-NG-1993) John A Mo. Department of Medical and
Physiological, Department of, Medical and Physiological Chemistry,
Nuarystan 3, Oppsaia, 71213, Sweden
1 (bases 1 to 285)
Mo.J.A., Bona,c.A. and Holndah.R.
Wariable region gene selection of immunoglobulin G-expressing B
cells with specificity for a defined epitope on type II collagen
14009207 Product\*\*immunoglobulin gamma heavy chain\*
//db\_xref\*\*PID\_9407815\*
/translation\*\*GalEVEVGASVTMSCKASGTFTSYRSHWVRQTDGGGLEWIGAI
TPGRODTSYRKFRGAMUTADUSSSTTROLSSLTSEDSAVYTCARGDVS\*
a 68 c 78 g 52 t Page 31 Page 29 8 Mon Apr 19 13:23:55 1999 gi07815
REYNORDS house mouse, 19G gene: immunoglobulin; variable region.
SOURCE house mouse, 19G gene: immunoglobulin; variable region.
REYNORDS house mouse, 19G gene: immunoglobulin; variable region.
REPERSON this musculus
REPERSON (PARTHORS HOUSE, MICHAELE, ROGENTIAL; ROGE RESULT 11
LOCUS MAIGGCVRD 303 bp RNA ROD 13-OCT-1993
DEFINATION M.nusculus immunoglobulin gamma heavy chain (DBA/1) gene, v region.
ACCESSION 225447 JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE REFERENCE AUTHORS TITLE RESULT 9
LOCUS
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ACCESSION
NID Apr 19 13:23:55 1999 KEYWORDS SOURCE ORGANISM Ouery Match 16.5; Score 76; DB 29; Length 302; Best Local Schilarity 93; Pred Bo. 236e-55; Length 302; Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps SdC gene V\_region 41 CTGGGGGCTCASTAMANTCCCTCAMAGCTTCTGGCTMCACATTACCASTACAMTA 100
98 CTGGGGCCTCAGTGMANTCTCCTCCAMGGCTTCTGCCTMCACATTACCAGTTACAMTA 157 SGS gene V\_region 158 TGCACTGGGTAAAGCAGGACACCTGGACAGGGCCTGGAATGGATTGGA Direct Submission Submitted (02-AUG-1993) John A Ho, Department of Medical and MATGGCYRF 290 bp RNA ROD 13-OCT-1993 M.musculus immunoglobulin gamma heavy chain (DBA/1) gene, v region %27451 neavy chain; IgG gene; immunoglobulin; variable region. nouse mouse. .7.A.

rect Submission

benitted (02-NGG-1993) John A Ho, Department of Medical and
ysiological, Department of Medical and Physiological Chemistry,
glaces I to 290.

chases I (bases 1 to 290)

...T.A., Bona.C.A. and Holmdahl.R.
riable region gene estection of immunoglobulin G expressing B
11s with specificity for a defined epilope on type II collagen
1.5. J. Immuol. (1993) In press organism="Mus musculus" strain="DBA/1" /db\_xref="tare-/dev --Location/Qualifiers product "Ammunoglobulin gamma heavy chain" db\_xref="FID:9407821" "translation="GAELVKPGASVKMSCKASGYTFTSYNHMVKQTPGQGLEWIGAI db\_xref="axon:10090"
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Lissus\_tyge="ymph node"
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rell\_the="critB334 hybridoma"
hydromamm="12" mitochondrial eukaryotes; Metazoa; Chordata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; lymph node" cell hybridoma" ICB391 hybridoma" US-08-836-455-3.xge US-08-836-455-3.rge 0

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BASE COUNT ORIGIN

77

SgS gene V\_region

gene-"IgG"

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Query Match
16.5%; Score 76; DB 29; Length 285;
Best Local Similarity 99.1%; Pred. No. 2.36e-55;
Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps

90 CTGGGGCCTENGTWARANTCTTCCANGCCTTCTGCCTNCACATTTACCAGTTACAATA 79

TGCACTGGGTAAAGCAGACACCTGGACAGGGCCTGGAATGGATTGGA 126

BASE COUNT ORIGIN

PPGNODTSTNOKFKGKATLTADKSSSTAYMOLSSLTSEDSAVYYCARGETGTG77 a 69 c 83 g 61 t

US-08-836-455-3.zge

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JOURNAL REFERENCE AUTHORS TITLE JOURNAL

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cir Substanton
sitted (OZANG-1993) John A Mo. Department of Medical and
stological Department of Medical and Physiological Chemistry,
stological Uppeal, 1013, Sweden
(Pages 1 to 202) and Rolation of immunoglobulin G-expressing B

, Bona, C.A. and Holmdahl, R. eregion gene selection of immunoglobulin G-expressing B this pecificity for a defined epitope on type II collagen number 23 (10), 2503-2510 (1993)

Location/Qualifiers
1. .302 /organism="Mus musculus" /strain="DBA/1" /db\_xref="taxon:10090" /dev\_stage="adult"

REFERENCE AUTHORS TITLE

U.A., Bona.C.A. and Holmdahl,R.

J.A., Bona.C.A. and Holmdahl,R.

Table region gene selection of immunoglobulin G expressing B

Libyth specificity for a defined epitope on type II collagen

J. Immunol. (1993) In press

ACCESSION

MMIGGCTRI 302 bp RNA ROD 13-OCT-1993 M.musculus immunoglobulin gamma heavy chain (DBA/1) gene, v region

940/828 940/828 NEWY Chain: IgG gene; immunoglobulin; variable region SOURCE house mouse.
ORCANISH Mus musculus Entrochondrial eukaryotes; Metazoa; Chordat; Enkaryotes; introchondrial eukaryotes; Metazoa; Chordat; Metazoa; Chordat; Metazoa; Me

mitochondrial eukaryotes; Metazoa; Chordata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;

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REYMORDS heavy chain; IgG gene; immunoglobulin; variable region.
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158 TGCACTGGGTAAAGCAGACCTGGACAGGGCCTGGAATGGATTGGA 204
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M.musculis mRNA for rearranged Ig heavy chain V region (J588
family 139MD 50c).
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Gliffilan, S., Fejiwara, H., Kilwahi H., Tohida, N., Anakwa, R.,
Benoise, G., Methis, D., Kalahimoto, T., Hek, T.W., and Rajvewy, K.
Somatic Pypermutation occurs in B cells of TdT, CD23, II-4, IgD and
CD30 deficient mouse mitants
Oppublished
Others 1 to 352): i
Nucler, N.,
Mether, N.,
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heavy chain; immunoglobulin superfamily; joining region; variable
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xtebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Ouery Match 16.5%; Score 76: DB 28: Length 305: Best Local Similarity 99.1%; Pred. No. 2.36e-55: Matches 106: Conservative 0: Mismatches 1: Indels 0:
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Submitted (02-A0G-1993) John A Mo, Department of Medical and
Physiological Department of, Medical and Physiological Chemistry,
Huastystan J Oppsala, 7313, Sweden
1 (Dates 1, Lo 105)
Mo, JA, Bonac, A. and Molndahl, R.
Wariable region gene selection of immunoglobulin G-expressing B
cells with specificity for a defined epitope on type II collagen
SILT, J. Immunol. 23 (10), 2503-2510 (1993)
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A. Roma,C.A. and Holmdahl,R.

Inlable region gene selection of immunoglobulin G expressing B inlable region gene selection of immunoglobulin G expressing B inla with specificity for a defined epitope on type II collagen in Limmunol. (1993) In press

[bases 1 to 305)
                                                                                                                                                                                                                                        /product*'immunoglobulin gamma heavy chain"
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Eutheria; Rodentia; Sciurognathi; Mycmorpha; Muridae;
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stage="adult"
sue_type="lymph node"

Ltype="B cell hybridoma"

Line="CIICB313 hybridoma"
                                                                                                                                                                   80 g 67 t
Gaps
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/db\_xref="taxon:10000"
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92 a 91 c 94 g 73 t 2 others

Cuery Match 16.5%; Score 6; DB 29; Length 352;
Best Local Similarity 9.1%; Pred No. 2.36e-55;
Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps

Db 101 TGCACTGGGTAAAGCAGACCTGGACAGGGCCTGGAATGGATTGGA 147

Oy 158 TGCACTGGGTAAAGCAGACACCTGGAACAGCTCGAATGGATTGGA 204

Memb470 355 bp RNA ROD 20-DEC-1996 M. museulus mEMA for rearranged Ig heavy chain V region (J588 family: 1294D.47c). antigen receptor; diversity region; immunoglobulin; immunoglobulin heavy chain; immunoglobulin superfamily; joining region; variable region.

s musculus Karyotae: mitochondrial eukaryotes: Metazoa: Chordata; Erebrata: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae;

(bases 1 to 355)

(ido.G., Jacobs, H., Reitring, H., Ruhn, R., Roes, J., Ruller, H., Iffilan, S., Fujkara, H., Kiutani, H., Toshida, N., Amakawa, R., Oolst, C., Mathis, D., Kishimoto, T., Mak, T. H., and Rajewsky, K. antic Nyparuntanion occurs in B cells of TdT, CD23, II-4, IgD and ID deficient mouse mutants

2 (Loses 1 to 355)

Nuclear M. Direct Submission

Direct Submission

Submitted (14-NW-1998) Nuclear M., Institute for Genetics at the

University of Cologne, Weyertal 121, Cologne 50931, Germany

1 (hases 1 to 355)

Texido G., Jacobs, H., Meiering M., Kuhh, R., Rose, J., Muller, H.,

Cirtilian S., Pujiwara, H., Kikhtani, H., Toshida, H., Anakawa, R.,

Benoist, C., Mathis, D., Kishimoto, T., Mak, T. M. and Rejevsky, K.,

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Ouery Match 16.5%; Score 76: DB 29; Length 355; Best Local Similarity 99.3%; Pred Box 236e-55; Matches 106: Conservative 0: Mismatches 1: Indels 0: Gaps

RESULT 15 LOCUS 1 DEFINITION 1 ACCESSION NID EYWORDS MMMD52C MANDESCE 358 bp RNA ROD 20-DEC-1996 M. musculius mRNA for rearranged Ig heavy chain V region (J588 family: 129MD.52c).

antigen receptor; diversity region; immunoglobulin; immunoglobulin region; variable region; variable house mouse. house mouse. Nus muscilus Bukaryotas; mitochondrial eukaryotes; Netazoa; Chordata; Vertebrata; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;

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Toxido G., Jacobs H., Meiering M., Rubn. B., Roes J., Nuller, H.,
Gilfillan, S., Fujiara, H., Kikuani, H., Kohdda, N., Amakevs, R.,
Benoist, C., Mathis, D., Kishimato, T., Hak, T.W. and Rajewsky R.,
Somatic Hypermutation occurs in B cells of TdT, CD23, IL-4, IgD and
CD30 deficient mouse mutants
Jupublished to 358)

Mon Apr 19 13:23:55 1999

Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

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REFERENCE AUTHORS Direct Submission Direct Submission the Congre Newscart Submission of Cologne Newscart 121, Cologne 50321, Germany Directory of Cologne Newscart 121, Cologne 50321, Germany Standard, Jacobs H., Meiering M., Kuhn, R., Roes, J., Muller, M., Chillian, S., Cujivara, H., Kikutani, H., Yoshida, M., Anakawa, B., Senolat, C., Mahlas, D., Kishimoto, T., Mah, T. H. and Rajevsky, K. Somatic hypermutation occurs in B cells of termal decomputional Cologne Standard Cologne Cologn

CD30-deficient mouse mutants Sur. J. Immunol. 26 (8), 1966-1969 (1996) 16350523

/organism=Wim masculus\*
/strain=19/5y\*
/note="partial v-b-7 region"
/db\_xrei="reason:10300"
/rearranged
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/roll\_type="198/gp positive B cells"
93 a 90 0 : 96 g /9 t

Ouery Match 16.5%; Score 76; DB 29; Length 358; Best Local Similarity 99.1%; Pred No. 2.36e-55; Length 369; Marches 106; Conservative '0; Mismatches 1; Indels 0; Gaps

AF025445

959 bp . DNA

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in (bases 1 to 358)
Texido G., Jacobs, H., Melering, M., Kuhn, R., Roes, J., Muller, W.,
Gliffilian, S., Rujiwara, H., Kikutani, H., Yoshida, H., Amakawa, R.,
Bendler, G., Mathlas D., Klahimoto, T., Mak, T. W. and Rajewaky, K.,
Sencits, M., Charles and B. cells of TdT, CD23, II.-4, IgD and
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BASE COUNT ORIGIN

Page 39

MOD Apr 19 13:23:55 1999

KEYWORDS SOURCE ORGANISM ACCESSION NID DEFINITION Mus musculus clone BHS2.19 immunoglobulin heavy chain variable region precursor gene, partial cds. AP025445 g2653851

REFERENCE AUTHORS TITLE

JOURNAL MEDLINE REMARK

Eukaryotee Metazea, Chordata; Vertebrata; Mammalia; Eutheria; Rodentas, Sciurognethi; Muridae; Murines; Mus. 1 (Dase 1 to Sibbs.A.J., Blanden; R.V. and Steele,E.J. Analysis of petterns of DNA sequence variation in flanking and coding regions of murine germ-line immunoglobulin heavy-chain variable gener evolutionsy implications proc. Matl. Acad. Sci. U.S.A. 91 (25), 12163-12157 (1994) 5508365

Trzetum: [[published erratum appears in Proc Matl Acad Sci U S A 995 ull 18;92(15):7135]} [[bases 1 to 959)

2 (based 1 to 959)
NorthorHub, H.S., Blanden, R.V. and Steele, E.J.
NorthorHub, H.S., Blanden, R.V. and Steele, E.J.
Sense and pseudogenes
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JOURNAL MEDLINE REFERENCE AUTHORS

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TITLE JOURNAL REFERENCE AUTHORS

(bases 1 to 958)

rele, G.P., Rothenfith, H.S., Sylstra, P., Gay, L.H., Averdunk, H.,
reele, E.J. and Blanden, R.V.

combination signature of garmline immunoglobulin variable genes

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(base) to 959)
Ller(G.P., Rethenfluh, H.S., Zylatra, P., Gay, L.M., Averdunk, H., sele, E.J., and Blanden, R.V.
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/organism="Mus musculus" /strain="BALB/c" /db\_xrefs=taxon:10090" /clone="BHS2.19" /chromosome="12"

germilne | oln(511 .514,697 .>959) | product\*'.lmmunoglobulin heavy chain | | preurpos. | oln(559 .614,697 .>959) | note\*"YHI66.2-related\* variable region

odon\_starrel roduct="immunoglobulin heavy chain variable region ecursor"

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AUTHORS TITLE JOURNAL

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Direct Submission
Submitted (14-MAY-1996) Musiler M., Institute for Genetics at the
University of Cologue, Neyertal 121, Cologue 59931, Germany
3 (bases 1 to 359)
Texido, G., Jacobe, H., Meiering, H., Kuhn, R., Ross, J., Ankuler, M.,
Gliffilan, S., Pujivara, R., Kikutani, H., Yoshida, N., Anakews, R.,
Senoist, G., Mathla, D., Kishimoto, T., Mak, T. M. and Rajewsky, K.,
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1. 358

/organism="Mus musculus" /strain="129/SV" /note="partial V-D-J region" /db\_xref="taxon:10090"

BASE COUNT ORIGIN /rearranged /cell\_type="IgM/IgD positive B cells" 94 a 92 c 92 g 78 t 2 others

Query Match 16.5%; Best Local Similarity 99.1%; Matches 106; Conservative Score 76; DB 29; Length 358; Pred. No. 2.36e-55; 0; Mismatches 1; Indels 0; Gaps

41 CTGGGGCTTAGTAMANTCCTGCAMGGTTTGGCTAGACATTTACCAGTTACAATA 100

RESULT 16 LOCUS 1 DEFINITION 1 MACHOLIC 358 bp RNA ROD 20-DEC-1956 M.musculis mRNA for rearranged Ig heavy chain V region (J588 tanily, 129DD.Ole).

ACCESSION NID KEYWORDS antigen receptor: diversity region; immunoglobulin; immunoglobulin beavy chain; immunoglobulin superfamily; joining region; variable region.

house mouse.

Mus musculus.

Eukaryotae; mitochondrial eukaryotes; Metaroa; Chordata;

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LOCUS MUSICH4C11 484 bp mRNA
DEFINITION Mouse 19H chain mRNA, VC region.
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MID alwara
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RESULT 20
LOCUS MOUV4114 453 bp | mRNA ROD | 20-APR-1995 | MOV | 20-APR-1995 | REFINITION NUM musculus immunoglobulin F9.13.7 heavy chain mRNA, partial cds.
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No. 2.36e-55; Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps
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Cheng H. T., Sood A. K., Ward R. E., Kieber-Emmons T. and Kohler H. structural basis of stimulatory anti-idiotypic antibodies 801. Immunol. 25, 33-60 (1988) 88147863
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1 (bezs 1 to 48) | Sood. A. K., Cheng. H. L. and Kohler. H. 
9 officient and general method for sequencing immunoglobulin mRNNs 
h. Efficient and general method for sequencing immunoglobulin mRNNs 
9. Immunol. Methods 95 (2), 227-235 (1996)
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Lecent J. Pelleyini, H., Souchon, H., Tello, D., Poljak, R.J.,
Peterson, N.C., Greens, H. I. and Alaszi, P. M.
Crystal structure of a cross-reaction complex between Fab F9.13.7
and Ghines-fowl lywoyme
J. Bloi. Chem. (1995) In press
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RESULT 21 LOCUS DEFINITION 1

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429 A 429

360 A 360

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U8-08-836-455-3.rge

Page 46

23-DEC-1997

Gaps

ACCESSION \$72514
NIP 9632698
EXPANDES
SOURCE
NHS SP. BALB/c spleen cell-Sp20 hybridoma.
ORGANISH Has Sp. Balb/c spleen cell-Sp20 hybridoma.
Dikaryotae; mitochondrial eukaryotes; Metasoa; Chordata;
V.a. cellorata; Dutheria; Rodentia; Sciurognathi; Muridae; Murinae;
V.a. cellorata; Decker, D.J., Eliman, N. RESULT 24
LOCUS 872514 RAD RRW, ROD 23-JAN-1995
DEFINITION anti-estradiol antibody heavy chain variable region (clone G3)
ACCESSION 872514 BALB/C, spicen cell-sP20 hybridoma, mRNA Partial, 361 ntl.
NID 9632698 Query Match
13.0%; Score 80; DB 29; Length 357;
Best Local Similarity 97.6%; Pred No. 2.16e-38;
Matches 120; Conservative 0; Miamatches 3; Indels 0; 369 TOTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAAGGACACCCCC 428 i (bases 1 to 381)
Stillman(A., Linton, P.J., Kouts, P.J., Decker, D.J., Klinman, N.R. and Gisnersa, T.R.
and Gisnersa, T.R.
Specific Liminogiobulin CDNA clones produced from hybridoma cell line and murine spiese for the specific collines are specification occurred. Direct Submission
Submitted (25-ARR-1996) D.G. Schindler, Weismann Institute of Schenes, Immunology, Rergi St., 76100 Rehovot, ISBARL Location/Qualifiers
1. 368 enBank staff at the National Library of Medicine created this The bases 1 to 357)
Nloch M. D. Alexander, A.L., Pippen, A.M., Pisetsky, D.S. and Cilbeson, G. Black and Street and Stree MUSY 357 bp mRNA ROD 07-JAN-1997 Mus musculus (cell line C3H/F2-20) chromosome 12 anti-DNA antibody heavy chain mRNA. Score 59: DB 29: Length 368; Pred. No. 2.37e-37; 0; Mismatches 0: Indels 0: Gaps U8-08-836-455-3.rge 1 others Page 47 RETWOODS Chnown.

SOURCE ORGANISM Chnown.

ORGANISM Chnown.

Chassified.

REFERENCE 1. Chass I to 360)

AUTHORS Shanis I. V. Northstein.A. and Ramjeesingh.M.

TITLE Use of antibody/antigen interactions to protect biologically active proteins and peptides

JORRAL Patent: US 3668579-A 14 11-NOV-1997;

LOCATION/QUALIFIERS

1. 1.560 "Auma" unknown" 79 t Mon KEYWORDS SOURCE DEFINITION ACCESSION BASE COUNT ORIGIN FEATURES Source ACTIONEDS have mouse.

OKCANISH His may chair immunoglobulin; variable region.

Dixaryota; Hetasa; Chordata; Vertebrata; Mammalia; Eutheria;

Reference: (Mases I to 369)

AUTHORS IN. Schindler.D.G., Lindner.A.B., Tavrik.D.S. and Bahbar.Z.

TITLE

TORGANISH TAVELED ACTIONED ORGANISM Query Match 12.8%; Score 59; DB 29; Length 381; Best Local Similarity 100.0%; Pred. No. 2.37e-37; Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps RESULT 23
LOCUS 20
DEFINITION M. musculus mENA for esterolytic immunoglobulin heavy chain variable region, isolate D2.4.
ACCESSION X27335 Apr 19 13:23:55 1999 RESULT 22
LOCUS
DEFINITION
ACCESSION
NID Query Match Best Local S Matches 5 QY 178 CCT 180 SGS gene MESTORVALA 304 bp mRNA ROD 23-MAR-1994 MAR MAR NOD WATER NOTION PARTIAL Cds. 1976 NOTION IN THE NOTION PARTIAL Cds. 198608 MAR NOTION PROCESSED GENE, VARIABLE REGION. THE MAR MAR NOTION PROCESSED GENERAL NOTION NOTION CONTROL OF MRNA. MAR NOTION PROCESSED AND STANDARD PROCESSED MAR NOTION CONTROL NOTION PROCESSED AND STANDARD PROCESSED AND STANDARD PROCESSED MAR NOTIONAL PROCESSED MAR NO Nutries 761.

1 (Pases I to 384)

1 (Pases I t entry (RCBI dubbed 153107) from the original journal article. This sequence comes from Fig. Sh. Location/Qualifiers 2 (bases 1 to 368) Schindler, D.G. 173311 360 bp DNA Sequence 14 from patent US 5686579. 173311 93009652 1 12.8%; Score 59; DB 22; Length 360; Similarity 100.0%; Pred. No. 2.37e-37; 59; Conservative 0; Mismatches 0; Indels 0; 100 /db\_xre(\*\*)PID:;632699\*
/translation:\*FOUNDESCRALINENGENINGCRASGIAFINVLIQMENGREGGG
LEWIGTINEGGGGTHYNEEREKGATITADESSTAIMGLSSGISDDSAVFFCARNYFY
ANDYMGGGTSYTSASAKTIPPSFYF
88 t
8 93 c 100 g 88 t /organism="Mus sp." /db\_xref="taxon:10095" nie "Anti-estradiol antibody heavy chain variable jion" "Ala esquence comes from Fig. 5A." oduct" anti-estradiol antibody heavy chain variable jion" anti-estradiol antibody heavy chain variable US-08-836-455-3.rge PAT

MOR

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121 CCT 123

BASE COUNT ORIGIN

/orgenism=\*Nus museculus. /strain='CSH/BcJ-Jpr/Pr-/stl.in="CSH/BcJ-Jpr/Pr-/sell\_type="bybridoma. /rissue\_Type="splen" 94 a 88 c 89 g 85 t

85 t

JOURNAL KEDLINE FEATURES SOUICE

Location/Qualifiers

TITLE

FEATURES Bource

CDS

anged type="hybridoma" asa ="Balb/c" =f="taxon:10090" ism="Mus musculus" te="D2.4" JOURNAL

Query Match 12.8%; Best Local Similarity 100.0%; Matches 59; Conservative

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Mol. Immunol 30 (14), 1295-1306 (1993) 94019421

Location/Qualifiers

BASE COUNT ORIGIN

/organism="Mus musculus" /db\_xref="taxon:10090" 96 a 96 c 100 g • 92

92 t

KEYWORDS SOURCE

REFERENCE AUTHORS TITLE

1 (bases 1 to 390)
Lohman, K.I. (bere), D.W., Carrillo, M.A. and Rennedy, R.C.
Characterisation of murine monoclonal anti-CDH; epitope
recognition, idiocope expression, and variable gene sequence

ocation/Qualifiers

/organisms "Mas musculus"
/strain-"BALS/c"
sub species-"domesticus"
/sub species-"domesticus"
/db\_tre:"taron,10090"
/tisus\_type-"5970.BALS/c fusion hybridoma"
/map"
/ma

LOCUS HUSL77IGHY 390 bp mRNA ROD 29-OCT-1994
DETINITION House hybridoma 1g rearranged H-chain mRNA V-region, partial cds.
ACCESSION M97876
NID 30-98678

V-region; immunogiobulin heavy chain; processed gene.
90URCE Hus mischius (strain BALS/c, sub\_species domesticus) 5920-BALB/c
ORGANISH Hus muschus democraticus (STATE CONTRA).

Bukaryotae: mitchicae.

mitochondrial eukaryotes; Metagoa; Chordata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;

Db 314 TGGACTRCTGGGGTCANGGANCTCACTCACCTCACCCAAAACGACACCCCA, 372
Oy 371 TGGACTACTGGGGTCANGGANCCTCAGTCACCCAAAAACGACAAAACGACAAAGAAACCCCA, 429

Ouery Match 12.8% Score 59, DB 29; Longth 384;
Best Local Similarity 100.0%, Pred No. 2,37-37; Longth 384;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps

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AUTHORS
TITLE
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KEYWORDS

SOURCE:

ORGANISH Homo sapiens eltochondrial eukaryotes; Hetazoa; Chordata;

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L (bases 1 to 401)

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KETWORDS samaa immunoglobulin; immunoglobulin.

SOURCE house mouse.

ORGANISH Mis musculing

Dikaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Muridae; Muridae
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LOCUS
DEFINITION
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Oy 371 TGGACTACTGGGGTMAGGAACACCACCTCTCTCTCAGCCAAAAACCACACCCCCA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION House mAB-15C5 mRNA for immunoglobulin gamma-1 chain, V-CH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compty Match 12.8%; Score 59; DB 29; Length 414; Best Local Similarity DOLON; Pred. No. 2, 275-37; Indels 0; Gaps Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps
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311 TGANCTACTGGGCTMAGGAACCTCAGTACCGTCTCCTCAGCCAAAACGACACCCCCA 429
371 TGANCTACTGGGCTMAGGAACCTCAGTACCGTCTCCTCAGCCAAAACGACACCCCCA 429
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9 Human uPA cDNA.
A18395
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PATENT: WO 911633-A 33 31-OCT-1991;
Location/Qualifiers
1 401
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/note="encodes FR4"
364, 414
364, 414
/gene="MGAVHC"
/note="CH1 region"
120 c 92 g
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/db_wref="taxon:9606"
12. 371
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Pred. No. 2.37e-37;
0; Mismatches 0; Indels 0;
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BASE COUNT ORIGIN

V\_region gene

/gene-lgH\*

RESULT 28
LOCUS
DEFINITION

CCESSION

APO06832 414 bp mRNA, ROD 02-OCT-1997 Nus musculus anti-slyvyrrhetic acid immunoglobulin heavy chain (MGANEG) mRNA, partial cds.
4F006832 92459929

RETWORDS
RETWORDS
SOURCE
Nouse mouse.
ORGANISM Mus muscullus
Elkaryotace mi
"artebrata; Me

PEATURES Source REFERENCE AUTHORS TITLE JOURNAL

/organiam\*\*Nus musculus\*
/attrin\*\*Balb/c
/db\_xref\*\*tuscn.10090\*
/cell\_line\*\*typeriamunized sples
/cell\_type\*\*slymphocyte\*
/cell\_type\*\*slymphocyte\*
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/coll\_type\*\*slymphocyte\*

spleen"

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/note="encodes FR1"
1. 294
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/note="VH3 family"
<1. >414

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misc\_feature misc\_feature

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KLEMGYLISYGSGSYNSSLASSKISITEDTSKKLEFFGANSYTTEDTAKYKCSTWGAN
\*TOTVVOTWGGGTSVTVSSAKTTPPSVYPLAPGSAA\*
91. 108

odon\_start+l roduct="anti-glycyrrhetic acid immunoglobulin heavy in"

CDS gene V\_region misc\_feature

/gene="MGAVHC"
(1. >414
/gene="MGAVHC"
/note="IGG1 IA"

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JOURNAL MEDLINE COMMENT

TITLE

US-08-836-455-3.rge

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mat_peptide 82. >>480 // note**19 gamma-1 chain*
BASE COUNT 121 a 119 c 126 g 114 t ORIGIN Chromosome 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.8%;
Best Local Similarity 100.0%;
Matches 59; Conservative
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g195078
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RO0687
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Construction and characterization of a recombinant murine
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mur. J. Blochem. 192 (3), 767-775 (1990)
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Vandamme, A.H., Bulens, F., Bernar, H., Melles, L., Lijnen, R.H. and
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to themRNA for the antibody MAISIS directed agains crosslinked human fibrin fragment D-diser to the Aragent D-diserved T-diserved T-dise
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(Dases I to 480)

(el.P., Huebner-Parajsz,C., Mattes,R., Lenz,H., Haug,H. and icamp.K.
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Location/Qualifiers
1. 480
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/translation="Cluterectisovolkosgpglyopsosisitctysgpslytyg
Yby:Rospekcleylcytysggstynnafishlsinkdnsksgyffkdnsloandta
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/codon_start=1
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LOCUS WUSIGHEP 480 bp mRNA ROD 01-SEP-1988
DEFINITION House Ig gamma-1 chain mRNA VC-region (VDJ4c) from hybridoma 1
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Matches 59; Conservative
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Score 59; DB 29; Length 444;
Best Local Similarity 100.09; Pred No. 2,378-37; Length 444;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps
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                                                                                              WINIGHTEEN 444 by RENA, ROD 30-JUN-1997 bouse Ig gamma-chain active v-region vDJ4c1 mRNA from hybridoma 14.13.2 v-H-81X family.

14.13.2 v-H-81X family.

14.13.2 v-H-81X family.

14.13.2 v-H-81X family.

14.13.2 v-H-81X family.

14.13.2 v-H-81X family.

14.13.2 v-H-81X family.

15.15.2 v-H-81X family.

16.15.2 v-H-81X f
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The framework region (FR) and complementarity determining region (CDR) boundaries are by homology from "Sequences of Proteins of Immunological Interest" (Rabat et al., NIH publication, 1983).

Location/Qualifiers

1. 501/Qualifiers
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Roca-Serra,J., Matthes,H.W., Kaartinen,M., Milstein,G., These,J. and Fougereau, Monocalonal Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT monocalonal antibodies. A paucisene system using alternate D-J recombinations to generate functionally similar hypervariable regions
EMBO J. 2, 867-872 (1983)
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Ver.D., Reis.M.H., Albanese,C., Costantini,F., Baltimore,D. and
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(BALB/C) anti-(ATT hybridoma GG oc 1.7 (spleen cells fused
VP-loma cell line X 63.Ag8:653), cDNA to mRNA, clone H IV 92
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/codon_gtart=1
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/thanslation="MKCSWVIFPLADVYGVHSEWOLOOSADLYKIGASVKLSCTAS
GERIKDTYIHWYGDEPOCLEWIGATIDLANGHTKIDFFLAKATTIDFPSKTAFPOL
58...>444
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Eutheria; Rodentia; Sciurognathi; Mycmorpha; Muridae;
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mitochondrial eukaryotes; Metazoa; Chordata;
; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                    Score 59; DB 29; Length 501;
Pred. No. 2.37e-37;
0; Mismatches 0; Indels 0; Gaps 0;
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Intrins, Aug. (Names 1 to 501)

Schiff, C., Hillilm. and Fougereau, M.

Interpretate of the murine anti-CAT response
Nucleic Acids Res. 11 (12), 4007-4017 (1983)

Data kindly reviewed (10-JAN-1986) by C. Schiff.

Location/Qualifiers

Sg

sig\_peptide

/organism="Mus musculus" /db\_xref="taxon:10090" <1..15

signal peptide

REFERENCE AUTHORS TITLE 8

371 TGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAAGGACACCCCCA 429

MAIGURI 501 bp RNA ROD - 30-MAR-1995 ROUSE MERNA for anti-CAT VH antibody heavy chain (Glu 60, Ala 30, Tyr 10); clone G8 Ca 1.7.

heavy chain; immunoglobulin; immunoglobulin heavy chain subgroup II; signal peptide; variable region.

yotae; mitochondrial eukaryotes; Metazoa; Chordata; Dzata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;

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                                                                                                                                                                                                                                                                                                                                                            processed gene.

SOURCE Mameralus (strain BALB/c, sub_species domesticus) cDNA to mRNA
ORGANISM Mus musculus

Bi Maryotae; matochondrial sukaryotes; Metazoa; Chordata;
Vertebrata; Entheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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DEFINITION Mus musculus IGC chain mRNA, VC-region, from hybridoma A23AA1.
ACCESSION 102346
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Raluza, B. Bettl.(S. Shao, H., Diamantstein, T. and Weidle, U.H.
A general method for chimerisation of monoclonal antibodies by
Inverse polymerase chain reaction which conserves authentic
S-terminal sequences
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Mrebrata; Euthería; Rodentía; Sciurognathi; Mycmorpha; Muridae;
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Location/Qualifiers
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/strain="BALB/c"
/stb_species="domesticus"
/db_xref="taxon:10090"
/cell_type="mature B cell"
74 124
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REFERENCE AUTHORS JOURNAL FEATURES SOUICE

> Location/Qualifiers 1. .536

CDS

ene="WM65 immunoglobulin gamma one"
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/organism="Mus musculus"
/strain="BALB/c"
/db\_xref="tazon:10090"
/tissue\_type="haemapoietic"
/ceil\_type="myloid/hybridoma"
/clone="PUC18"

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WM65 immunoglobulin gamma one" Uregion" WM65 immunoglobulin gamma one" v region" 143 WM65 immunoglobulin gamma one" D region" REFERENCE AUTHORS TITLE JOURNAL

ect Submission mitted (08-FEB-1931) R. Seymour, Haematology Dept, St Vincents pital, Victoria St, Sydney NSW 2010, Australia |Passes 1 to 536) | poir.R.

rryotae; mitochondrial eukaryotee; Metazoa; Chordata; .ebrata; Butheria; Rodentia; Sciurognathi; Myomorpha; Muridae; .nae; Mus.

SOURCE ORGANISM NID KEYWORDS

RESULT 35
LOCUS MN
DEFINITION M.
ACCESSION X5

MMIGMM65B 536 bp RNA
M.muegulus WM65 immunoglobulin gamma one

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constant region; Ig kappa chain; Ig variable region; unoglobulin.

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Oy 371 TGAACTACTGGGGTZLAGGAACCTCAGTCAGCTCAGCCTAAAACGAGACGCCCCA 429
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DEFINITION Artificial construct constant region.
ACCESSION A23165
AVID 9641653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Overy Match 12.8; Score 59, DB 22; Length-588;
Best Local Similarity 100.0; Preds No. 2,7e-37; Length-588;
Matches 59; Conservative 0; Minatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.8%;
Best Local Similarity 100.0%;
Matches 59; Conservative
                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303 TEGACTACTROGGETENAGGALCCTAGTCACCGTCTCCTCAGCCAMAACGACACCCCCA 361
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Mus musculus antibody heavy chain
000927
g437093
                                                                                                                                                                                                                                                         (base 1 to 660)
entscher S.L.
free Submission
ubmitted (10-NUG-1993) Susan L Deutscher Dr., Blochemistry,
niversity of Missouri-Columbia, M121 Medical Sciences Building,
Columbia, MD, 65212, USA
Location/Qualifiers
1. 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 12.8%;
Similarity 100.0%;
59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               7, 77-83 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  on and characterization of nucleic acid-binding antibody to from autoimmune mice-derived bacteriophage display
                                                                                                                                                                         /organism="Mus musculus"
/etrain="MRL/lpr"
/db_xref="taxon:10090"
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/ftanslation="IESGGPELVREGASYRMSCKASGYPETSYVMHWYROKPOGYRPYYA
                                                                                                                                   /tissue_type="spleen"
<1. .>660
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*Cranslation**PRRIPHISTHPPOAX**
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RELTSEDTAVYTCARGGFFYGNDYWQGGTSVTVSGAXTTPPSVFPLAPS*
191. 345 /
191. 345 /
191. 345 /
191. 346 /
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Pred. No. 2.37e-37;
0; Mismatches 0; Indels 0; Gaps
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Pred. No. 2.37e-37:
0: Mismatches 0: Indels 0: Gaps
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FAB mRNA, partial cds.
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                                                                                                                                                                                                                                                                                                         KEYMORDS
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KEYMORDS
Has muscultus
OKCANISH
Kis muscultus
Dikkryotee: mitochondrial eukaryotes; Hetazoa; Chordata;
Elkaryotee; mitochondrial eukaryotes; Hordata; Chordata;
Wertentata; Futheria; Rodentia; Sciurognathi, Myomorpha; Muridae;
Wertentata; Futheria; Rodentia; Sciurognathi, Myomorpha; Muridae;
Wertentata; Futheria; Rodentia; Sciurognathi, Myomorpha; Muridae;
Wertentata; Geo.

ATTILE
Sciurognatia; Scholatod, A.D., Jahang G. and Karu, A.E.

TITLE
Sciurognatia; Scholatod, Totalia; Scholatod, A.D., Lingae; Sciurognatia; Sciurognati
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LOCUS
DEFINITION
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MMU04352 669 bp mRNA
Mus musculus Biozzi anti-diuron
mRNA, partial cds.
U04352
g600715
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Mus musculus
Eukaryotae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 12.8%;
Similarity 100.0%;
59; Conservative
            /organism="Mus musculus"
/strain="Biozzi"
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504 TGACTHOTOGGGTCHAGGALACCTCAGTCAGCCCALAAAGGACACCCCA 562 3 (Cases 1 to 631)
Ware J. and Ruygeri.E.M.
Direct Submission
Submitted (19-78E-1997) Molecular and Experimental Medicine, The
Scripps Research Institute, 10550 Morth Torrey Pines Road, La
John CA 90107, USA
Location/Qualifiers
1. 631 MMU90237 631 bp mRNA Nus musculus anti-von Willebrand factor mRNA, partial cds. U90237 I (bases 1 to 631)
Pojanusa, Y. Dammi, Y., Titani, K., Niinomi, K., Nishio, K., Takase, T.,
Toshioka, A. and Pikir, Millabrand factor (vWF) monoclonal antibody
Studies on anti-von Willabrand factor (vWF) monoclonal antibody
NMC-4, which inhibits both ristocetin and botrocetin induced vWF
binding to platelate (1)(poprotein 1b

binding t Mus musculus Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Chases 1 to 631)
TE-JJ and Buggest E.M.
Ti-von Willebrand factor monoclonal antibody NWC-4, heavy chain munopibobiin coding sequence published NDYRGOGISUTVSSAKITPBSVVPLAGSAAGINSAVTLGGLVRGYFPEPVTVTNNSG SLSGVHTFPAVLGSDLYTLSSSVTVPSSTWPSETVTCHVALFASSIKVDKKIVPROC 15 a 191 c 166 g 147 t . (10 late(= PDI) 91890344. Vermalallon = polymeroslatictyrotarii (vrupadigatichi)ali Vergotaveslaseilei tedeskovezlonslootarii (vrupadigatichi)ali Vergotavetyroslatiendevyreagsalvestootarii (vrupadigatichi)ali Sooveteraviosdiltilssovepestyroslatichi /organism="Mus musculus"
/db\_xref="taxon:10090"
/cell\_type="hybridoma"
(1...>631 /note="anti-vMP monoclonal antibody" (codon\_start=2 (product="anti-von Willebrand factor antibody NMC-4 heavy-chain" US-08-836-455-3.rge ROD 17-MAR-1997 antibody NMC-4 heavy chain

Page 64

Score 59; DB 29; Length 660; Pred. No. 2.37e-37; 0; Mismatches 0; Indels 0; ROD 28-MAR-1996 Ig heavy chain V and CH1 regions Gaps

2 (bases 1 to 669)
2 (bases 1 to 669)
Rell.C.W. A., Scholthof, K.G., Zhang, G. and Karu, A. E.
Recombining the control of duron: A model for the phenylurea
combining site
(fin) Melaon, J.O., Karu, A. E. and Woog R.B. (Eds.);
DETHNOLMENTSIS OF AGROCHEMICALS: EMERGING TECHNOLOGIES: 50-71;
CCS Symposium Series 586, American Chemical Society, Washington DC
1995)

3 (Name 1 to 669)
Bell.C W.
Bell.C W.
Boinet Submission
Submitted (14-08C-1993) Christopher W. Bell. CWR Bybridoma
Facility, Oxforestry of California, Berkeley, 1030 San Pablo Ave.
Albany, CA 9016-08. USA
Location/Qualifiers
1. 6697/Qualifiers

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ğ
Apr 19 13:23:55 1999
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89

/cell\_type="hybridoma, IgGl kappa" /tissue\_type="spleen, hyperimmunized" <1. .>669

odon\_start=1
coduct="anti-diuron immunoglobulin heavy chain V and CH1

\_xref="PID:g600716" inslation="LESGGGLVI

14.110="1-lesgeluepogs.K.Lecaasgetesuyghtwyraaperglew SSTITKADYRGRETISRDYAKTLELANTSLREDTANTYCARBOTTVSGH WRGCTSVTVSSAKTTPPSVYBLAGGAAQTRSWTTLGCLUKATYPEVFTV SGVHTPPAVLASDLYTLSSSVTVPSSTWPSQTVTCNVAHPASSTKVDKKIVP

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'db\_xref="taxon:10090"
'clone="pl12.2"

BASE COUNT ORIGIN

misc\_feature misc\_feature misc\_feature misc\_feature

/note="CH1 region" 151 a 196 c 173 g

149 t

/note="CDRH3" 358. .649 /note="CDRH2" 203. .325 /note="1 136: .1

CDRH1

RESULT 41 LOCUS DEFINITION

KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE

synthetic construct.
synthetic construct.
synthetic construct
artificial equence.

1 (bases 1 to 792)
1 (bas

CCESSION

APO78800 791 bp BRNA SYN 03-AUG-1998 Synthetic Mus musculus single chain anti-HIV-l Rev variable fragment BRNA, complete cds.
APO78800 9337580

Db 317 TGARTACTGGGGTCAAGAACCTCATCACGGTCTCCTCAGCCAAAACGACCCCCA 375
Oy 371 TGARCTACTGGGGTCAAGAAACCTCAGTCACCGTCTCCTCAGCCAAAAACGACACCCCA 429

12.8% Score 59; DB 29; Length 669; Best Local Similarity 100.0%; Pred. No. 2, 37e-37; Matches 59; Conservative 0; Hismatches 0; Indels

0; Indels 0;

Caps

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US-08-836-455-3.rge

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Page 66

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RESULT 42
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LOCUS ED843-
DEFINITION CDNA-6
ACCESSION E0843-
NID 9917-65
REYWORDS JP 199
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00-007-1997 (Rel. 52, Created)
00-007-1997 (Rel. 52, Lat updated, Version 1)
Mouse anti-CEA Page Chain gene
JP 198315312-A/2, Version 1990
Has muscilus (house mouse)
EMBATYOLE, Metacos (Chordets, Vertebrata; Mammalia; Eutheria; Rodentia;
EMBATYOLE; Metacos (Chordets, Vertebrata; Mammalia; Eutheria; Rodentia;
Chiaryole; Muscaco; Chordets, Muscaco; Muscaco; Chordets, Muscac 332 TGACTACTGGGTCAAGAACCTCAGTCACCTCTCTCAGCCAAACGACCCCA 390
311 TGACTACTGGGTCAAGAACCTCAGTCACCTCTCTCAGCCAAACGACCCCCA 429 hitymitymeru K., Heruberuto R.H., Ulriamu E.H., Aasaa D.R., tonarudo B.O., tonaru 15-NUG-1985
15-NUG-1985
16-NUG-1985
16-NUG-1985
168-NUG-1989
168-NUG-1 inN/Op.cimninp,(cimp21/00,cimninp); randedness.bouble; pology: Linea; pohetical: No: il.sense: No: standard; RNA; ROD; 1528 BP

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BASE COUNT ORIGIN

1. 1347 /organism="unknown" 341 a 381 c 335 g 290 t

Ouery Match 12.89; Score 59; DB 22; Length 1347; Best Local Similarity 100.04; Pred. No. 2.78-37; Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps

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Page 67

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PEATURES source BASE COUNT ORIGIN CC anti-sens FH Key FH source FT source FT source FT FT OTR onti-TWY-antibody;

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Location Qualifiers

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1. 155 /organism="unidentified" /db\_xref="taxon:32644" 386 a 450 c 372 g 345 t anti-sense: No; Key 1. .1553
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Matches 59; Conservative 0; Hismatches 0; Indels Length 1553; 0; Gaps

MESULT 45
LOCUS 173745
DEFINITION Sequence 17 from patent US 5686600.
ACCESSION 173745
NID.\_\_\_\_ 93009886 PAT 23-DEC-1997

ATTORNES

SOURCE

ORGANISM Unknown.

ORGANISM Unknown.

Declaration

Declaration

Declaration

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Declaration

Declaration

TITLE

AUTHORS

AUTHOR

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Query Match 12.8%; Score 59; DB 22; Length 1797;
Best Local Similarity 100.0%; Pred. No. 2.37e:37;
Matches 59; Conservative 0; Mismatches 0; Indels 0;
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Apr 19 13:23:55 1995
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JOURNAL MEDLINE REFERENCE AUTHORS TITLE 2 (Asses 868 to 1848) Jennings M.P. and Beacham, I. R. Analysis of the Escherichia coil gene encoding L-asparaginase II, ansb, and its regulation by cyclic AMP Receptor and FNR proteins J. Bacteriol. 172, 1491-1488 (1990)

3 (eites)
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Ramjesaingh, M., Zyvulko, M., Rothstein, A. and Shami, E.Y.
Romoclonal antibodies can protect L-asparaginase egainst
Bacetivation by typsin
Asparanology (N.Y.) 10, 442-445 (1992) es 1 to 1848)

JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL

- Submission tited (18-FEB-1994) Wayne J. Newsted, University of Guelph, likar Biology and Genetice, Guelph, Ontario, NIG 2W1, Canada Location/Qualifiers /organism="synthetic construct" /db\_xref="taxon:32630" 1. .360

misc\_feature /mote\*immunoglobulin light chain variable region cloned from Mab 12-4 cell line; raised to asparsginase\* (clation=[3]) e="single-chain antibody" .1848

gg

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/Codon\_act+t-1
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/Tennil\_

misc\_feature misc\_feature misc\_feature /note="immunoglobulin heavy chain variable region cloned from Mab 12-4 cell line; raised to asparsginase" /clation=[3] 766. 867 ion="flexible linker" 765

'note="double flexible linker"

Page 71

Mon Apr 19 13:23:55 1999

misc\_feature

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968..1846
//gene\*angs\*
//gene\*a

gene

BASE COUNT ORIGIN /gene="ansB" | 398 t

Ouery Match 12.8%; Score 59; DB 32; Length 1848; Best Local Similarity 100.0%; Pred. No. 2.37e-37; Matches 59; Conservative 0; Mismatches 0; Indels 0; 6/5 Teachthoreagnethaealaceteaencheonthoreagnalaceacanacacaca, 733
8/7 Teachthoreagnethaealaceteancheonthoreacacanacacacacacacaca, 829
8/7 Teachthoreagnethaealaceteancheonthoreacacanacacacacacaca, 829 Gaps

bequence.

PAT

08-JUL-1993

RESULT 48

A07700
DEFINITION Synthetic ploifs DNA accession A07700
NID 9413186

ACCESS-NID
SETWORDS
SOURCE
ORGANISH unidentified.
ORGANISH unidentified.

DEFRENCE 1 (basesified.

AUTHORS Redolp.R. Juchner/J. and Leng.H.
AUTHORS Redolp.R. Juchner/J. and Leng.H.
DORRAL Patent. EP 0364950Minant antibodies expressed in P DORRAL Patent. EP 0364950Minant antibodies expressed in P DORRAL Patent. AUMIEJN GMSH.

DORRAL Patent. AUMIEJN GMSH.

1. July Market 1500;
DORRAL PATENT GMSH.

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prokaryotes

Query Match 12.8%; Best Local Similarity 100.0%; Matches 59; Conservative 568 TRANSPARTIGUEGREMAGRAMACTEMBERGEGETTCCTEMBERGAMACGACACCCCCA 626
371 TRANSPARTIGUEGREMAGRAMCCTCMBTCMBTCTCMBTCTMAMACGACACCCCCA 429 Score 59: DB 22: Length 3343; Pred. No. 2.37e-37; 0: Mismatches 0: Indels 0: Gaps

RESULT

49

Page 69

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Page 70

RESULT 46
LOCUS
DEFINITION S
ACCESSION 1
NID g3009653 173512 1848 bp DNA Sequence 15 from patent US 5686579. 173512 PAT 23-DEC-1997

REFERENCE AUTHORS TITLE KEYWORDS SOURCE ORGANISM 

JOURNAL FEATURES Source

BASE COUNT ORIGIN Ouery March 12.8%; Score 59; DB 22; Length 1848; Best Local Similarity 100, 00; Pred No. 2, 176-177; Length 1848; Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps

RESULT 47

LOCUS 106941 1848 bp DNA SYN 18-FEB-1985
DEFINITION SYNthetic chimeric immunoglobulin-L-asparginase II gene, partial cds.
ACCESSION 05943

REPORDS

APPROXIS

APPROXIMATION

APPROXI Engineering resistance to trypsin inactivation into L-asparaginase through the production of a chimeric protein between the ensyme and a protective single-chain antibody Unpublished

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LOCUS
LOCUS
ACCESSION ADDRA
EXPRISES unidentified
ORGANISM Unclassified
ORGANISM Unclassified
ACCESSION ADDRA
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AC E09029;
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ORIGIN
Search completed: Sat Apr 17 17:14:46 1999 Job time: 1659 secs.
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                                                                                                                                                                                                                                                                                        Ouery March 21.44; Score 57; DB 10; Length 399; Best Local Similarity 100.04; Pred. No. 280e-35; Matches 57; Conservative 0, Mismatches 0; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
Sequence 399 BP: 106 A: 102 C: 105 G: 86 T: 0 other;
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DNA sequence of monoclonal TSH antibody, gamma chain.
A07558
g413070
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/codon_ckartel
/codon_ckartel
/product='fragment of monoclonal TSH antibody, gamma
/bain
/db_xref="PDD:g413072"
/db_xref="PDD:g4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard: RNA: ROD; 399 BP.
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/notes*Tranment 3 of heavy chain variable region of Idio3*
region of Idio3*
/notes*CDR3 of heavy chain variable region of Idio3*
ature 32.38
/notes*Tranment 4 of heavy chain variable region of Idio3*
Location/Outlitters
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HEGINARE H., ADSILME Y.;

*ALTERO ACTH SEQUENCE OF ART: IDIOTYPE ANTIBODY TO ANTI-CANCER HUMAN NONCOLONAL ANTIBODY AND DNA BASE SEQUENCE CODING FOR THE SAME:

BACKER NUMBER: TP 1995101999-AVI.

OS RUM BANGALLUM (CRUME)

DY 1995101999-AVI.

PP 1095101999-AVI.

DP 108-DRI-1993 APT 19932772950

PP 106-COTT-1993 APT 19932772950

PP 106-COTT-1993 APT 19932772950

PP 106-COTT-1993 APT 19932772950

PR 106-COTT-1993 AP
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08-007-1997 (Rel. 52. Latt uddated, Varsion 1)
08-007-1997 (Rel. 52. Latt uddated, Varsion 1)
cDM, encoding heavy chain variable region of mouse antiidiotype
antibody named iddo against CLM-1gG idiotype.

JP 1995101999-JAI.
Mus musculus (house mouse)
Eukaryota, Mesacoa; Chordets; Vertebrata; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridas; Murinas; Mus.
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/tissue_type="Spleen"
/cione="3GB1"
1. 27
28. 399
133...174
Poster*Fagment 2 of heavy chain variable region of Idio3*
175.0225
225 of heavy chain variable region of Idio3*
                                                                                                                                                                                                                                                                     118. 1132 ------
/mote="CDR1 of heavy chain variable region of ddos"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26. 1999
Zot. "Heavy chain variable region of mouse antidotype antidotype antidody named Idio3 against CLN-IgG didotype"
                                                                                                                                                                                                                                                                                                                                                                                                           //ote="Fragment1 of heavy chain variable
region of Idio3"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U. Distribution rights by Oxford Molecular Ltd Unit.

Run on: Tabular output not generated. MParch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm Sat Apr 17 17:15:13 1999; MasPar time 629.71 Seconds
1310.996 Million cell updates/sec

Title:
Description:
Perfect Score:
N.A. Sequence:
Comp: >US-08-836-455-3
(1-461) from US08836455.eeq
461 1 ATGGAATGCAGCTGGGTCTT......
TACCTTACGTTGGACCCAGAA.....

. CTGGTCCCTGGAAGCTTGGG

461

Scoring table:

Database: Searched: Post-processing: Nmatch STD embi-est/5

1.em\_est/2.em\_gss/3:em\_gss/4:em\_gss/3

1.em\_est/2.em\_gss/3:em\_gss/4:em\_gss/3

5.9b\_est/6.ep\_est/0.7:eb\_est/1.8:eb\_est/2.9:eb\_est/1.3

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1.0:pb\_est/1.1::pb\_est/1.2::pb\_est/6.2::p Minimum Match O% Listing first 1000 summaries Dbase 0: Query 0 TABLE jmetric Gap 60 2275026 seqs, 895388244 bases x 2 Mean 8.690; Variance 1.210; scale 7.180

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Geisel.S., Kucaba.T. Lacy.M., La.M., Martin.J., Morris.M.,

Geisel.S., Willer T., Leenon.G., Boares,B., Wilson,R. and

Materston, Mylia-T., Lennon.G., Boares,B., Wilson,R. and

The Reabl-HRMI Mouse EST Project

ALL Uppblabrad (1996)
                                           LigarG., Clark,M. Shith,S., Meek,S., Warmer,S., Umrania,Y., BligarG., Clark,M. Shith,S., Meek,S., Warmer,S., Umrania,Y., Williams,G. and Brenner,S.

Blinct Submitted (18-PEB-1997) KRC Human Genome Mapping Project Resolution: Hinton, Cambridge, CB10 18B. Email: biohelpehymp.mrc./ Vector: pBluescript II KS

"Lype: Phagemid Files. KS
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Fugu rubripes.
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Vertebrate: Actinoppersydi: Neoptersydi: Peleostei; Euteleostei;
Acanthopterydi: Percomorpha; Tetraodontiformes: Tetraodontoidei:
Tetraodontidae: Fugu.
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One pass dye-terminator sequencing of cosmid cloned genomic sequence.
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This clone is available royalty free through LLNL: contact the
TMAGE Comsortium (info@mage.llnl.gov) for further information.
NGI:91508
Seq primer: -Sell3 rev2 ET from Amersham.
Location/Qualifiers
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Weshington Diversity School of Medicinep
Weshington Diversity School of Medicinep
4444 Forest Park Parky, Box 8501, St. Louis,
7el: 314 286 1810
Fax: 314 286 1810
Email: mousestevetton.vustl.edu
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Best Local Similarity 95 8%; Pred No 7.79e-48;
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MashI-HBH Mouse EST Project

MashI-HBH Diversity School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, NO 63108

- Tel: 314 286; 880

Par: 314 286; 880

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buman clones/66/28 prime; "Ti lirary seares melhocyte 2mbH vectorspi?TiD (pharmacia, with a modified polylinker heartming (ampicillin resistant) Raitel-Not I Raitel-Not R Male. Lat strand CDN was primed with a Not I oligo(df) primer (but in the construction of the Not I and cloned the Not I and Sco (pharmacia), digested with Not I and cloned into the Not I and Sco RI sites of a modified prily vector (pharmacia). Library Constructed by Benio Source and M.Fatina Bosaldo. NRA from normal tops with melanocytes (#53/4) was kindly provided by Den Anthony P.
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MGI:678249
Seq primer: ~28ml3 revl ET from Amersham
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/db_xref="taxon:3103"
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NISW Pigu rubripes

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Hablington Oniversity School of Medicine

444 Forset Park Parkway, Box 8501, St. Louis, MO 63108

Tol. 114 286 1800

Pax: 314 286 1810

Easil: erfecteon west.edu

High quality sequence atops: 385

Source: IMAG Consortium, LiAN

This clone is available rayaity-free through LiAN; contact the
This clone is available rayaity-free through LiAN; contact the
Location/Qualifiers

Location/Qualifiers

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                                                                                                                            humin clone-27989 primeremil -00 forward library-Scares multiple science is albester vector pr771D (bharmacia) with a modified polylinker V.TPE. phagesid hose-WHOB (ampicilin resistant) Raitza-Rot I maitza-Rot I maitza-Rot I maitza-Rot I maitza-Rot I maitza-Rot I maitza-Rot I colsgo(dr) primer primerry structured CDN was primed with a Not I - oligo(dr) primer i maitza-Rot I maitz
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y/80006 al komo sapjens cDNM clone 279899 3' similar to 9b:H62505
CHALONAPHYLATOXIN CHEMOTACTIC RECEPTOR (HDMAN);.
H41009 12164607
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes:
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/dev_stage="6-8 month old"
/dev_stage="6-8 month old"
/lab.host="SOLR (kanamycin resistant)"
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/clone_lib="Stratagene mouse lung 937302"
/sex="female"
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Page 28

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ss 10-DEC-1997 genomic survey sequence

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2 others

Mon Apr 19 13:23:57 1999  Sarcopterygii, Choanata, Tetrapoda, Anniota, Hammalia, Theria, Archania, Finestes, Catarrhini, Hominidae, Homo, AUTHORS Hilleria, Clark, M., Dubque, T., Elliaton, K., Havkins, M., Butanan, M., Euranan, M., Euranan, E., Elliaton, K., Havkins, M., Halland, M., Euranan, E., Elliaton, K., Havkins, M., Halland, M., Euranan, E., Elliaton, K., Havkins, M.,
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/organisme\*Homo sapiens\*
/clone=\*279899\*
<1. .>433
149 a 80 c 65 g 139

Query Match 4.3%; Best Local Similarity 100.0%; Matches 20: Conservative Score 20; DB 19; Length 433; Pred. No. 3.62e-08; O; Mismatches O; Indels

BASE COUNT ORIGIN

65 g 139 t

Length 433;

0 Gaps FEATURES Source

RESULT 0 Al16120 552 bp mRNA EST 14-MAY-1897
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ACCESSION AL16126 (HUMAN); mRNA sequence.

ACCESSION AL16127 ETWOODS ET.177

Romo aspiens Elharyotae: mitochondrial eukaryotes; Metasoa; Chordata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae;

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188 CCCTGTCCAGGTGTCTGCTT

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RESULT 9
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DEFINITION ACCESSION NID REYWORDS SOURCE ø H47534 478 bp mRNA PROBAGE 1935 EST 16-AUG-1995 PP.EF2\_CAREL P29691 ELONGATION PACTOR 2;. 16-AUG-1995 EST. 2923366

REFERENCE AUTHORS Enharyotes: Metacos; Eumetazos; Bilatería; Goelomata;
Deuterostemia Condeda; Verrebrata; Goathostomata; Osteichthyes;
Sarcopterygii; Choanaka; Verrebrata; Goathostomata; Osteichthyes;
Euthería; Archonta; Primates ettapoda; Amilota; Mammalia; Theria;
I (bases 1 to 478) Primates Cetarthini; Rominddee; Romo,
Hillstr,L. Clark, M., Dibuque, T., Eliston, K., Hawkins, M.,
Holman, M., Hulman, M., Kucaba, T., te M., Cancon, J., Marra, M.,
Parsons, J., Rikin, L., Rohlfing, T., Soares, M.,
Toryaskis, E., Waterston, R., Hillamson, A., Rohldman, P., and

ORGANISM

The WashU-Merck EST Project Unpublished (1995)

FEATURES source Contact: Wilso Rt
Washington Oniversity School of Medicine
444 Force: Parkray, Box 8501, St. Louis, Mo 53108
Te: 314 286 180
Par: 314 286 180
Par: 314 286 180
Danil: estewation.wustl.edu
Estewation. Fish quality and the sequence stops: 35
Source 18 Available royalty-free through LIMI; contact the 1946S Consortium (LIMI; Fish quality and the sequence stops: 35
This close is available royalty-free through LIMI; contact the 1946S Consortium (LIMI) and the sequence stops: 1946S Consortium (LIMI) and the seque

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/organism="Homo sapiens" /clone="193528" a 134 c 123 g 120 t

6 others

Page 31

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ACCESSION AA88463.

NEWHOODS 9293983
SCHEEP COMMISS.

ORGANISM Rome sapiens Chordata; Vertebrata; Mammalia; Eutl Pidaryota; Metasoa; Chordata; Vertebrata; Mammalia; Eutl Pidaryota; Mammalia RESULT 10 LOCUS DEFINITION AA884453 208 bp mRNA EST 27-MAR-1998 ajStad0 si Soeres testa NRT Homo sepiens cDNA clone IMAGE:1194774 3 similar to TR:008810 008810 U5-116KD. ;, mRNA sequence.

Eutheria;

Project (CGAP),

Contact: Robert Strausberg, Ph.D.
Tel: (201) 196-1150
Badi: Robert\_Strausbergenih.gov
cDM, Libsort\_Strausbergenih.gov
Bonaldo, Pry Perparation: M. Sento Soares, Ph.D., M. Patima
Bonaldo, Pry Perparation: M. Sento Soares, Ph.D., M. Patima
CDM, Albrary Attrayed by: Greg Lenon, Ph.D.
DM, Sequencing by: Wankington University Genome Sequencing Center
Close Sequencing Mr. NCT-GGAP close distribution information can be
found through the I.M. G. E. Consorting Contact
found through the I.M. G. E. Consorting Contac

Prace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq priner: -60ml3 fwd. Er from Amersham
High quality sequence stop: 1.
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1. .208

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POTYD Pac (Pharmacia) with a modified poblylinker; Site, 1: Not I: Site, 2: EGO RIL lst strand CDNA was prepared from mBNA obtained from (Counteeth the Laboratories, Inc., and primed with a Not I oligo(d7) primer [5]

US-08-836-455-3.rst

Page 30

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Page 29

REFERENCE AUTHORS

| These | to 55) | Hilliston, K., Havkins, M., Plantist, C. (Lark, M., Dubuque, T., Elliston, K., Havkins, M., Rolman, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifffin, J., Rochiffin, T., Tan, F., Trevakis, E., Washungton, R., Hilliamson, M., Nohldmann, P., and Wilson, R., Washungton, R., Start, P., San, P., San, P., San, P., San, R., Washungton, R., Washun

Contact: Wilson RX Washington University School of Medicine 444 Protest Park Fathway, Box 8501, St. Louis, MO Tel. 314 286 1810 Par: 314 286 1810 Eart: 1312 286 1810

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Examil: extension vustleds
This clone is available royalty-free through LLNL; contact the
TRAGE Consortium (infostmags.lnl.gov) for further information.
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FEATURES Source

/ Organium='Romo saplens'
/ Organium='Romo s

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Ouery Match 4.3%; Score 20; DB 6; Length 552; Best Local Similarity 100.0%; Pred. No. 3.62e-08; Matches 20; Conservative 0; Mismatches 0; Indels 354 CCCTGTCCAGGTGTCTGCTT 373 0 Gaps

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Page 34
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EST$3370 Jurkat T-cells V Homos sapiens cNWA 5' end similar to
hypothetical protein (GB:DZ1183), mRWA sequence.
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1 (bases to 210)

Hillar, L., Alten, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

Kucaba, T., Laey, M., Le, N., Lemnon, G., Marra, M., Martin, J.,

Kooce, B., Schelachezy, K., Steptoce, M., Tan, F., Theising, B.,

White, T., Wylte, T., Waterston, R. and Wilson, R.

Wash-Merck EST project 1997

Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1800 PARWay, Box 8501, St. Louis, MO 63108
Tex: 314 286 1810
Email: estekaton vuetl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: estfwatson.wustl.edu
This clone is available royalty-free through LINL; contact the
TMAGE Consortium (info@image.nlnl.gov) for further information.
Seq primer: -28ml3 rev4 gr from Ameraham.
__contion/vbulifiers
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Initial assessment of human gene diversity and expression patterns based upon 83 million nuclectides of CDNA sequence Matture 377 (6547 Suppl), 3-174 (1995)
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DEFINITION EST13453 Testis tumor Homo sapiens cDNA 5' end similar to similar

ACCESSION AA428970 NID 92110596 KEYWORDS EST. PEATURES source Apr 19 13:23:57 1999 0ery Match 3.9%; Score 18: DB 25; Length 225; Best Local Similarity 100.0%; Pred. No. 1.05e-04; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps The Institute for Genomic Research
712 Medical Center Drive, Rockville, MD 20850 USA
713 Medical Center Drive, Rockville, MD 20850 USA
713 3018899425
Tax: 3018899425
Email: arkelavetigr.oro
For clone avaitation nomb.

2 (hases 1 to 256)

Adams, M.D., Kerlavsger, A.R., Fleischmann, R.D., Fuldner, R.A., B., Adams, M.D., Kerlavsger, A.R., Fleischmann, R.C., Man Hall, G., Goosyne, J.D., Edwick, G., Goosyne, J.D., Chite, G., Sutton, G., Blake, J.A., Brandon, R.C., Man Hall, G., The, L.D., Chite, G., Sutton, G., Blake, J.A., Brandon, R.C., Man Hall, G., The, L.D., Fleiger, A.J., Fill, R., Gotton, M.D., Barther, B., Googlagen, R.S., Golder, M., Googlagen, R.S., Googlagen, R. Contact: Kerlawage, AR
Bicinformatics
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The Institute for Genomic Research
1712 Medical Conter Drive, Rockville, MD 20850 USA
1712 Medical Conter Drive, Rockville, MD 20850 USA
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1715 human. Komo sapiens Eukaryotse; Mstazoa; Chordata; Vertebrata; Mammalia; Eutheria; Bomo aspiens Bukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrate; Mammalia; Butheria; Primates; Catarrhini; Kominidae; moglobulin gamma arkerlayetigr.org additional sequence and expression to availability, additional sequence and expression tion related to this EST, please check the Tick Ruman Gene http://www.tigr.org/cdb/ngi/hgi.html)
incr: MiJ Reverse. /db\_xref="ATCC (inhost):155470"
/db\_xref="taxon:9606"
/clone\_lib="jurkst T-cells V"
/cell\_type="T-lymphocyte"
<1. .>225 Organiam\*Homo aspiens\* (/note\*\*Organ: testia; Vector: pBluescript SK-; Site\_1: EcoNI; Site\_1: Xho1s (Mb\_rref\*\*Arcc (lihost):192398\* /db\_rref\*\*arco:9606\* /organism="Homo sapiens" /note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI" 3 Reverse. ion/Qualifiers Reverse. on/Qualifiers 54 g 54 t V(III) region, mRNA

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ACCESSION NID RESULT 14
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DEFINITION

AAS6019 267 bp BRMA 21-APR-1997 EST19376 Lymph node I Homo sapiens cDNA 5' end similar to immunoglobulin gamma 4 heavy chain, C region (CB:KO12116), mRNA

REYWORDS SOURCE ORGANISM

ologo sapiena Sulkaryotae: mitochondrial eukaryotes: Metazoa; Chordata; Sertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;

REFERENCE AUTHORS

Bobo.

E 1 (bases 1 to 267)

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Bill.C.J. tues. H. B., Kirkness E.F., Weinstock, K.G., Gocayne, J.D., Will.C.J., tues. H. B., Kirkness E.F., Weinstock, K.G., Gocayne, J.D., Will.C.J., tues. H. B., Kirkness E.F., Weinstock, K.G., Wan-Wal-C., Weinston, E., Gocayne, J. F., Helbon, E., Weinston, D.T., Pelligtion, S. M., Keiley, J.W., Keiley, J.C., Liu, T., Marchan, T.A., Collins, E.J., Weinston, E., Weinston, J.F., Li, Y., Weinston, E., Weinston, J.F., Li, Y., Weinston, T. W., Weinston, J.F., Weinston,

US-08-836-455-3.rst

Query Match 99%; Score 38; DB 24; Length 256; Best Local Similarity 100 0%; Pred No. 108-004; Dender 0; Mismatches 0; Indels 0;

/clone\_lib="Testis tumor"
/sex="male"
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/dev\_stage="adult"
<1...>256
52 a 83 c 72 g 46

Page 37

Mon Apr 19 13:23:57 1999

Page 38

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Page 39
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Deutarostoria; Chorakas, Verebrada; Gosthostomata; Ortsichthyes;
Sarcopterygii; Chosakas; Terapoda; Amilota; Mamalia; Theria;
Entheria; Archorata; Primates; Cetarrifan; Romidake; Romo.
1 (Names; Ito 354).
Hillier; L. Clark, W., Dubuque, T., Ellaton, K., Harvins, M.,
Bolman, M., Hitman, M., Tucoba, T., Lanco, C., Marra, M.,
Parsons, J., Hilfani, Rochaf, T., Soner, M., Tun, P., and
Wilson, R., Waterston, R., Williamson, A., Wohdman, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other_ESTs: TRC168590
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomi.
9712 Medical Center Driv.
Tel: 3018699056
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Unpublished (1995)
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Adam, M.D., Kriaveg, A.R., Pleischmann, R.D., Fuldner, R.A.,
Adam, M.D., Kriaveg, A.R., Pleischmann, R.D., Fuldner, R.A.,
Balt, C.J., Lee, N. H., Kirkness, A.F., Weitscock, K.G., Googyne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, N.C., Mant, A., C.,
Clayron, R.A., Cline, T.R., Cotton, M.D., Earle-Haghes, J., Fise, L.D.,
Clayron, R.A., Cline, T.R., Cotton, M.D., Earle-Haghes, J., Fise, L.D.,
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/clone="182528"
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dical Center Drive, Rockville, MD 20850 USA
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// All Arter taxon: 1605:
// Clone_11in=Lymph node I*
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  revaluation org additional sequence and expression on related to this EST, please check the TIGR Human Gene ttp://www.tigr.org/tb/hgi/hgi/html)
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Pitegerald.L.M., Fitebudy, M.M., Fritchman J.L., despingen, M.S., Glodek, A., Gebma C.L., Manna M.C., Hebboar B., Mink R.P. L.M., Melley, J.M., Kelley, J.C., Lib, L.T., Manneron, S.M., Mirkey, D.M., Meron-Palanques, R.F., McDonald, L.A., Nuyuen, D.T., Pallinger, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, S.M., Small, K.V., Spriggs, T.A., Utterback, T.R., Methan, J.F., Li, Y., Bednarik, D.F., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D.F., Regg, D.F., Ferrite, A., Facher, C., Hastings, G.A., Me, W., Ha, J.S., Geene, J.M., Grubs, J.F., Hudson, P., Kim, A.K., Kappind, L., Mel, M., Mel, Mel, M., Mel, Mel, M., Mel, Mel,

95026280 Other\_ESTs: THC168356 Contact: Kerlavage, AR

titute for Genomic Research dical Center Drive, Rockville, HD 20850 USA

reerlayeigr.org additional sequence and expression ion related to this EST, please check the TIGN Human Genettp://www.tigr.org/tdb/hgi/hgi.html)
ef: M1) Severe.

ocation/Qualifiers

Overinium="Romo mapiens"
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Query Match 3.9%; Best Local Similarity 100.0%; Matches 18; Conservative

Score 18; DB 25; Length 308; Pred. No. 1.05e-04; 0; Mismatches 0; Indels

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3.9%; Score 18; DB 16; Length 354

Best Local Similarity 100.0%; Pred. No. 1.05e-04; Matches 18; Conservative 0; Miamatches 0;

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Page 42

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LIAM HODD SAPIERS

CENTRALES MECASOA: Chordata: Verrebrata: Grathostomata; Mammalia:
EURLTYCHE MECASOA: Cherrithii Moninidee; MomoEN Hiller L. Clark M. Dubuque T. Elliston K., Hawkins M.,
EN Hiller L. Clark M. Dubuque T. Elliston K., Hawkins M.,
EN Hiller M., Multhan M., Kucaba T. T. An F., Trevaskins M.,
Waterston R., Williamson M., Wohldmann, P. and Wilson, R.
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WashT Merch Merch Merch Merch Merch Merch Merch Merch Merch Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; imates; Catarrhini; Hominidae; Homo. information can be Page 43 Š RESULT 20 N42612 406 bp mRNA 125-1AN-1996 DEFINITION SYLEDGL-11 Homo sapiens CDNA clone 27079 5 similar to ACCESSION N42612. BASE COUNT ORIGIN ACCESSION
NID
NETWORDS
SOURCE
ORGANISM RESULT 18 ACCESSION NID REYWORDS SOURCE FEATURES source REFERENCE AUTHORS Apr 19 13:23:57 1999 Query Match 3.9%; Score 18; DB 10; Le Best Local Similarity 100 0%; Pred. No. 1 05e-04; Matches 18; Conservative 0; Mismatches 0; Best Local Similarity 100.0%; Pred. No. 1.05e-04; Matches 18; Conservative 0; Mismatches 0; ORGANISM Albino.

BUMAryotae; Hetazoa; Eumetazoa; Bilateria; Coelomata; Osteichthyes; Deuterostonia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Barcoprezygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Arbonta; Primates; Caterrihin; Henhidde; Homeria; 1 (bases 1 to 405)

Billier; L. Clark, N., Dubuque, T., Elliston, K., Havkins, M., AA128970 389 bp mRNA, EST 37-1EC-1997 EOOBALZ :I Stratagene neuroepithelium HTZRAMI 93734 HOmo aspiens CDNA clone 567070 5' similar to TR:G434755 G434755 MRNA;, mRNA High quality sequence stop: 393. bloom apiens

Bikaryolae: Metasoa: Chordata: Vertebrata: Hammalia: Eutheria:
Primates: Catarriini: Rominidae: Romo.

(base 1 to 389)

Hillier, L. Clark, N. Dubuque, T. Elliston, K., Havkins, N.,

Bolman, M., Halman, M., Ruenba, T., Le, N., Lennon, G., Marra, M.,

Parsons, J., Rikin, L., Rohling, T., Tan, P., Trevaskis, E.,

Parsons, J., Rikin, L., Rohling, T., Tan, P., Trevaskis, E.,

Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.,

Washd-Merck Egy Project

Unpublished (1995) sequence. AA128970 g1688753 EST. This clone is available royalty free through LiML; contact the IMAGE Comporting (including LiML) or further information. Seq primer: -28Hi3 rev3 from Amerikan High quality sequence stop: 311. Location/Qualifiers 1. J89/Qualifiers Content: Wilson RK
Washington University School of Medicine
4444 Forest Park Farhway, Box 8501, St. Louis, KO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: estewates vusti.edu
Emai human clone=270799 primer=77 library=Soares melanocyte 2RbHN vector=p771D (Pharmacia) with a modified polylinker hose-p81000 (ampicillin resistant) Rattel-Rot I sattel-Roc Rattel-Roc II sattel-Roc I 167042 /db\_wret="taxon:900"
/clone=!hoc::08526a;
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/fiden=\_tip="RCI\_COAP\_Gaa!"
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//or /organisam=Homo sapiens\*
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/force: Cloned unidirectionally. Primer: Oligo dT. NT2
/force: Cloned unidirectionally. Primer: Oligo dT. NT2
/force: Cloned by State Length 399; Indels Indels 0 ::

Page 44

Mon

Apr 19 13:23:57

FEATURES Source

BASE COUNT ORIGIN

/organism="Homo sapiens" /clone="60240" a 107 c 36 g 127

Query Match

3.91;

Score 18; DB 5; 36 g 122 t

Length 356;

REFERENCE AUTHORS

ORGANISM

RESULT 17
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DEFINITION
ACCESSION
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g648082

T40458 356 bp mRNA EST ya01901.82 Homo sapiens cDNA clone 60240 3'.

08-FEB-1995

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RESULT 19 LOCUS DEFINITION

AA594034 399 bp mRNA nn18908.sl NCI\_CGAP\_Gasl Homo sapiens mRNA sequence.

CDNA clone IMAGE:1085246,

Gaps

0

Query Match 3.9%; Best Local Similarity 100.0%; Matches 18; Conservative

Score 18; DB 11; Length 389; Pred. No. 1.05e-04; 0; Mismatches 0; Indels

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Gaps

REFERENCE AUTHORS TITLE

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Elkaryotee; Metasoà; Chordata; Vertebrata; Mammalia; Eutheria;
Plantes; Cabarrildi; Rominidae; Romo.
(Chaes to 199); il ini.nih.gov/ncicgap.
NCI-CGAP http://www.iobi.nlm.nih.gov/ncicgap.
Mational Cancer antitute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997); ;

Tel: (30) 466-1850 i.

Bail Rober\_Straubergfish.gov

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Base Proviement: L. Jeffrey Medeiros, M.D., Michael R.

Base Proviement: L. Jeffrey Medeiros, M.D., Michael R.

Base Proviement: L. Jeffrey Medeiros, J.D.

CDM Library Preparation: Stratagene, Inc.

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Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550//

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ACCESSION NID

AA594034 92409384

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SOURCE Cyprinus carpio peritoneal exudate cells cDNA to mRNA.
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WashDystor Exp Project
WashIngton University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohifing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. Wilson,R. Wilson,R. The WashO'Herrk EST Project Unpublished (1995)
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Cyprinus carpio alginate-induced 48 h peritoneal
L29, mRNA sequence.
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(ampicilin resistant) ReitelsWot I Raite2=EgoRI last arrand CDNN
vas primed with a Not I - oliop(dri) primer [5] RI last arrand CDNN
young constructed with a Not I - oliop(dri) primer [5]
double-stranded CDNN was aize selected, lighted to Ego RI adapters
(Pharmacia), digested with Not I and cloned into the Not I and Ego
rometructed by Sento Soarse and K.Fatima Bonaldo.

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LOCUS R84038 A21 bp mRNA clone 249835 5' similar DEFINITION yv88ell.rl Rome saptens cDNA clone 249835 5' similar ACCESSION H84038 SP.EZ_CAEEL P29891 ELONGATION PACTOR 2:
ACCESSION H84038 H84038 P1052709
NID 91052709
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                         Query March 394; Score 10: DB 19: Length 435; Best Local Similarity 100 04; Pred. No. 105-04; Marches 18: Conservative 0; Mismatches 0; Indels 0;
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Deutrontomia Chordata; Vertebrita; Ginthostomata; Ostedchthyes:
Barcopterytii; Choanata; Tetrapoda; Jamiota; Mamalia Bristis;
Eutheria; Arbona; Primates; Catarthini; Monidae; Monidae;
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Hilleria; Catark, Dibuque, T., Ellston, K., Havkins, K.,
Hilleria; Catark, N., Dibuque, T., Le, M., Lennon, G., Mazza, H.,
Passons, J., Rittin, L., Solates, M., Canon, G., Mazza, H.,
Passons, J., Rittin, L., Solates, M., Whidmann, P. and
Wilson, B., Waterston, R., Williamson, A., Wohldmann, P. and
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 suppression subtractive hybridization technique subinhed only in Database (1998) In press prisk, R., Rakou, M., Shin, D. and Tano, T. Stibses 1 to 489) Stipk, R., Rakou, M., Shin, D. and Tano, T. Stipk, R., Shin, D. and Tano, T. Shin, R.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RX
WashU-Merck EST Project
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/organiam="Cyprinus carpio"
/ob_xref":taxon:7962:
/ob_xref":taxon:7962:
cell_type="peritoneal exudate cells"
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/clone="214375"
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0; Mismatches 0; Indels
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AVVIA 9840350 EST. human clone=153980 library=Soares breast 2NbHBst vector=pT7T3D

30-MAY-1995 similar to

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Page 49

Mon Apr 19 13:23:57 1999 LOCUS DEFINITION US-08-836-455-3.rst GSS 25-JUN-1998 genomic clone 2290H4,

Page 50

RESULT 26 LOCUS DEFINITION FEATURES source FEATURES source ACCESSION NID NEYWORDS SOURCE REFERENCE AUTHORS REFERENCE AUTHORS Apr 19 13:23:57 1999 ORGANISM ORGANISM Contact: Wilson RK
WashIp Merch EST Project
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WashIp Merch Est Parkway, Box 8501, St. Louis, MO 63108
WashIngton Diversity, Box 8501, St. Louis, MO 63108
WashI State How WashInd Was 25 Contact: Milson RK
WashU-Mero RK
WashU-Mero RSI Project
WashU-Mero RSI Project
WashIngton University School of Medicine
WashIngton University School of Medicine
WashIngton University School of Medicine
Tel: 314 286 2010
Fax: 314 Deuterostonia, Chordata, Veriebrata, Coelomata, Deteichthyes: Barcopterygii, Chordata, Veriebrata, Gnathescomata, Osteichthyes: Barcopterygii, Chomanta, Tetrapoda, Anniota; Mammalla, Theria; Eutheria, Archonta, Printers, Paraboda, Anniota; Mammalla, Theria; Loses 1 to 449)

Hillier, L., Clark, M., Dubuque, T., Elliston, K., Hawkins, M., Bolman, M., Hiltman, M., Ruchas, T., Le, M., Lennon, G., Marra, M., Pareons, J., Riftin, L., Rohlfing, T., Soares, M., Tan, F., Pareons, J., Riftin, L., Rohlfing, T., Soares, M., Tan, F., areas, M., Matterton, R., Hillamson, A., Wohldmann, P. and The Wash-Herck EST Project H43391 - 449 bp mRNA 257 . 31-70L-1995 yp09907 r1 Hamo saptems crobk clone 186972 5 similar to spreez 1872 cror p09445 ELONGATION FACTOR 2 ; 5 similar to 9919443 grown factor 2 ; 5 similar to 9919443 grown factor 2 ; 5 similar to 9919443 Eukaryotes, Metson, Eunetanes, Bilteria, Coelomata, Osteichthyes, Deutarostesia, Chordata, Vertebrate, Goathecata, Osteichthyes, Sacopterydi, Chonnata, Tetrapoda, Anniota, Mamalia, Theria, Eutheria, Atonica, Prinates, Cetarriai, Cotarria, Cotarri The WashU-Merck EST Project Unpublished (1995) 'NOTINCEANTYMANATOGAGEGGGCGCCTTTTTTTTTTTTTTTTT'; ),
double-stranded oDNA was ligated to Eco RI adaptors (Pharmacia), addgested with Not I and cloned into the Not I and Eco RI sites o' modified pTTJ vector (Pharmacia), Library went through one round of normalisation to a Cot \* 310, Library constructed by Bento goarse and M. Festina Bonatok US-08-836-455-3.rst Gaps

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RESULT B BASE COUNT ORIGIN Ouery Match 39, Score 18: DB 15; Length 439; Best Local Similarity 100 0%; Pred No. 105e-04; Matches 18: Conservative 0; Mismatches 0; Indels 0; 

M On Apr 19 13:23:57 1999

Page 51

US-08-836-455-3.rat

ACCESSION M73311 457 bp mRNA TITLE ST 07-APR-1996 TYTLC11.r1 Homo septems CDNA clone 248180 5 similar to SHEPZ\_CAREL P29691 ELONGATION FACTOR 2 :.
W73311 F1330435

ORGANISM 

REFERENCE

The WashU-Merck EST Project Unpublished (1995)

Page 52

PEATURES

BASE COUNT ORIGIN

/organism="Homo sapiens" /clone="186972" a 124 c 111 g 119 t

4 others

Query Match

3.9%; Score 18; DB 16; Length 449;

AQ004108 442 bp DNA CIT-HSP-229084.TF CIT-HSP Homo sapiens genomic survey sequence.

Eukaryota Metaroa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarthini; Hominidae; Home I (bases 1 to 442) Adams, M.D., Roussley; S.D., Fledd, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Mible, C., Shisuya, H., Simon, M. and Verter, J. C., Dies of a random BAC End Sequence Database for Sequence-Ready Map

REFERENCE AUTHORS

TITLE

REYWORDS SOURCE ORGANISM

NID NCCESSION

Unpublished (1997)
Other\_GSSs: CIT-HSP-2290H4.TR
Contest: MARY Adams
Department of Enkaryotic Genomics
The Institute for Genomics
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: 944-945

Email: mdadamsttjgr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tlgy.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html seq primer: Mi-01; class: bAC endds.

FEATURES source

Location/Qualifiers
1. 442
/organism="Romo eapiens"
/organism="Romo eapiens"
/note="ector: pBeloBACII; Site\_1: HindIII; Site\_2:
HindIII"

BASE COUNT ORIGIN 164 a /db\_xref="taxon:9606" /clone="2290H4" /clone\_lib="CIT-HSP" /esy="Male" /cell\_type="Sperm" /cell\_type="Sperm" 124 t

Query Match 3.9%; Best Local Similarity 100.0%; Matches 18; Conservative Score 18: DB 27: Length 442: Pred. No. 1.05e-04: 0: Mismatches 0: Indels 0: Gaps

문

Best Local Similarity 100.0%; Pred. No. 1.05e+04; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps

RESULT 27
LOCUS
DEFINITION

Gentect: Wilson RK Washington University School of Medicine Washington University School of Medicine 4444 Forest Park Parkey, Box 8501, St. Louis, NO 53108 Fal: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1810
Sanil: estemateon washington Child Source: IMAGE Consortium, LiMI Source: IMAGE Consortium (Infosinsse: Lini.gov) for further information. IMAGE Consortium (Infosinsse: Lini.gov) for further information. IMAGE Consortium (Infosinsse: Lini.gov) for further information.

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Mon Apr 19 13:23:57 1999
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Tel: 114 286 1800

Fax: 114 286 1810

Fax: 114 286
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BASE COUNT
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AUTHORS
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LOCUS
DEFINITION
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3.9%; Score 18: DB 20; Le
Best Local Similarity 100.0%; Pred. No. 1.05e-04;
Matches 18; Conservative 0; Mismatches 0;
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Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
                                                                                                                                                                                                          Wilson,R.
The WashU-Merck EST Project Unpublished (1995)
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/organism="Homo a
/clone="248180"
<1. >457
105 a 129 c 112
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1172.r1 Homo sapiens cDNA clone 182447 5' similar
EPZ_CAEEL P29691 ELONGATION FACTOR 2;
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ACCESSION
NID
KEYWORDS
SOURCE
ORGANISM

REFERENCE AUTHORS TITLE

human.

Homo sajiens

EDNaryota: Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Primates; Catarriini; Hominidae; Homo.

Mc1 Chass 1 to 482)

Mc1 Coda) Hers://www.nobi.nlm.nih.gov/ncicgap.

Mc1 Coda) Achord finstitute, Cancer Genome Anatomy Project (CGAP).

Tunco General Anatomy

Unpublished (1997)

RESULT 29
LOCUS
DEFINITION

A1125673 462 bp mnWh. EST 03-SEP-1998 OLGG09 x1 Seate\_NSP\_PS\_98\_V0T\_PA\_P\_S1 Know sapiens cDNA clone mquence. Sequence of the control of the c

BASE COUNT ORIGIN

/organism="Homo sapiens"
/clone="182447"
98 a 129 c 111 g 122 t

1 others

Query Match Best Local S Matches 1

h 3.9%; Score 18; DB 16; Length 461; Similarity 100.0%; Pred. No. 1.05e-04; 18; Conservative 0; Mismatches 0; Indels 0;

Gaps 0 FEATURES source

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US-08-836-455-3.rst
Page
   55
                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Tel: (201) 196-1350
mail: Robert-Strausbergenih.gor
This clone is available royalty-free through LLNL; contact the
IMAGE Connortium (infodiange.llnl.gov) for further information.
High quality sequence stop: 407.
Location/Qualitiers
/organium="Romo aspiens"
```

FEATURES source

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Mon Apr 19 13:23:57 1999
                                                                                                                                                                                                                                                                                     COMMENT
RashD-Merch RET Project
Washington University School of Medicine
444 Forest Park Parkvay, Bx 8501, St. Louis, NO 63
Tel: 314 266 180.0
Fax: 114 266 180.0
Fax: 114 266 181.0
This clone is available royalty-free through LLNL; .
TMAGE Consortium (infostmage.linl.gov) for further is
Seq primer. JBml sevy Br from Amersham
High quality acquence acop: 434.
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estéwateon wusti.edu one is available royalty-free through LLNL; contact the one is available royalty-free through LLNL; contact the onestimm (info@mage.llnl.gov) for further infomation.mer: -8m13 rev2 ET from Ameraham loostion/Qualifiers 11.464

/Organisms\*Homo sapiens\*
/Organisms\*Homo sapiens\*
/Organisms\*Homo sapiens\*
/Organisms\*Homo sapiens\*
polylinher; Sit=2.1 Not I; Sit=2.1 Eco RI; let strand cDNA
polylinher; Sit=2.1 Not I; Sit=2.2 Eco RI; let strand cDNA
polylinher; Sit=2.1 Not I; Sit=2.2 Eco RI; let strand cDNA
(Co.Eprepared from mRNA obtained from pooled 8-9 week
(Co.Eprepared Sit Manuel on Boo RI adaptor
(Pharmeta), digested with Manuel on Rivers
(Pharm

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Query Match
Best Local Similarity 100.0%;
Matches 18; Conservative
Score 18; DB 7; Len
Pred. No. 1.05e-04;
0; Mismatches 0;
                                                Length 464;
                                Indels
                                 0
                                Gaps
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BASE COUNT ORIGIN

1 (Panes 1 to 464)
Hiller.L. Allan.M. Bowler.L. Dubuque,T., Geisel,G., Jost,S.,
Mocaha,T., Lory,M., Le,R., Lennon,G., Marra,M., Marrin,J.,
Moora,B. Goballenberg,K., Steptoe,H., Tan,F., Thelsing,B.,
White,Y., Whis,T., Waterston,R. and Wilson,R.
MasDiplerch Egy 7; Saterston,R. and Wilson,R.
Unpublished (1997)

RESULT 31 LOCUS DEFINITION

KEYWORDS SOURCE ORGANISM

ACCESSION NID

REFERENCE AUTHORS

RESULT 30
LOCUS
DEFINITION

Db 443 ACATCTTCACTGAGGCCC 460

Query Match 3.9%; Best Local Similarity 100.0%; Matches 18; Conservative

Score 18; DB 17; Length 462; Pred. No. 1.05e-04; 0; Mismatches 0; Indels

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BASE COUNT ORIGIN

/note="Cogan: pooled: Vector: p773D-Pac (Pharmacia) with a modification of page 1. Not I. Site 2. Boo RI. Equal cancel polylinker: Site 1. Not I. Site 2. Boo RI. Equal cancel polylinker: Site 1. Not I. Site 2. Boo RI. Equal cancel page 1. Not I. Site 2. Boo RI. Equal cancel page 1. Not I. Site 2. Boo RI. Equal cancel page 1. Not I. Site 2. Room 1. 
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FEATURES source NID KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE EST.

common foe plant:

desembryanthemum crystallinum

kesembryanthemum crystallinum

gukaryotae, Viridiplantae; Charophyta/Embryophyta group;

Embryophyta; Tracheophyta; seed plants; Hagnollophyta;

hagnollopsida; Caryophyllales; Aisoaceae; Hesembryanthemum.

1 (bases 1 to 474)

Cushman, J.C.

Cushman, J.C. Contact: Cushman JC
Department of Bloobenistry and Molecular Biology
Oklaboma State University
150 Mobile Research Center, Stillvater, OK 74078-3
150 Mobile Research Center, Stillvater, OK 74078-3
150 Mobile 160-744-5207
151 405-744-799
152 405-744-799
153 140-744-799
154 140-744-799 An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum Unpublished (1997) ". IO-1 row: D column: 9

Trimer: Mil reverse

quality sequence step: 350.

1. 473 "Nesembryanthenum crystallinum\*
//nore-"Vector: Lambda Uni-Zap XX, Bluescript SX-; Site\_1:
ZooRi: Site\_2 xhoi:
ZooRi: Site\_2 xhoi:
//oloe="Lot-15" row plant Lambda Uni-Zap XX expression
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//tione\_1bb="Lot-2 plant Lambda Uni-Zap XX expres OK 74078-3035,

Query Match Best Local & Matches h 3.9%; Score 18; DB 11; Length 474 Similarity 100.0%; Pred. No. 1.05e-04; 18; Conservative 0; Mismatches 0; Indels Length 474; o; Gaps 0

8 B 32

N40313

474 å BRNA

EST

**8** ₽ Apr 19 13:23:57 101 GGGCCTCAGTGAAGATGT 96 1999 US-08-836-455-3.xst

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RESULT 33 LOCUS DEFINITION ACCESSION AloO7469 476 bp mRNM.
AloO7471 IZ-UTW-1998
LO-J7ZHIJR Ke plant Lanbad Uni-Zap XR expression library. O bours
Wacl treatment Mesembrynnthemum crystallinum cDNA clone Id-372 5/
similar to photosystem I reaction center protein subunit N
precursor (Pash), mRNA sequence.

REPYREMS

SOURCE

COMMISH Hesembryanthenum crystallinum

ORGANISH Hesembryanthenum crystallinum

Dikaryota: Viridiplantae: Charophyta/Embryophyta;

Embryophyta: Trachosphyta: deed planta; Magnoliophyta;

eudicoryledons: Caryophyllidae: Caryophyllales; Airoaceae;

REFERENCE 1 (Pases 1 to 476)

AUTHONS Cashann, J. C. 476)

AUTHONS Cashann, J. C. 476) common ice plant,

FEATURES source Concent: Cushman JC
Department of Blockenistry and Molecular Biology
Okaha Stdft University
Solobia Stdft Solobia Stdft Solobia
Staff Solobia Stdft Solobia Stdft Solobia
Staff Solobia Stdft Solobia Stdf **NSD** 

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Mon

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141 a

89 c

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138

US-08-836-455-3.rat

BASE COUNT ORIGIN Query Match 3.9%; Best Local Similarity 100.0%; Matches 18; Conservative Score 18; DB 15; Length 476; Pred. No. 1.05e-04; O; Mismatches O; Indels . Gaps 0

RESULT 34
LOCUS
DEFINITION ACCESSION NID . AA426145 495 bp mRNA EST 16-OCT-1997 aviic01.rl Scares NRHMPu S1 Homo sapiens cDNA clone 768964 5' similar to TR:G392018 G392018 FILAMIN. ;, mRNA sequence. AA426145 G392018 G392018 FILAMIN. ;

KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS Homen appins

Rome appins

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Rome appins

Romen to 459

Hillier L. Allen M. Bowles L. Dubuque T. Geisel G. Jost S.,

Romen T. Lery M. Ley M. Lennon G. Marra M. Martin J.,

Moore B. Schlichberg K. Steptoe M. Tan.P. Theising B.,

White Y. Wile T. Waterston R. and Wilson R.

Washower to Project 1997

Unpublished (1997)

FEATURES source

organiam\*Romo aspisna\*
(notem Corgan inted (see below), Vector: p7773D-Pac
(notem Corgan inted (see below), Vector: p7773D-Pac
(pharmacia) with a modified polylinker: Site\_1: Not I;
(pharmacia) with a modified polylinker; Site\_1: Not I;
(pharmacia) interest products of placeid DNA program uterus
(pharmacia) and detail heart (mellays) were stated and as circles
(pharmacia) in witho (pollowing MA) purification (in 18 DNA

were made in witho (pollowing MA) purification (in 18 DNA) a subtractive hybridization vas PCR-amplified cDNAs from pools of

Page 57

Mob

Apr 19 13:23:57 1999

Page 58

yx80f07.rl Homo sapiens cDNA clone N40313

DEFINITION ACCESSION HID KEYWORDS SOURCE

westor-pg771D (pharmacia) with a modified polyliner hose-pM189 (ampiciliin resistant) Raitel-Not I Raitel-Pco RI Male. lat strand cDM was primed with a modified polyliner hose-pM189 (in resistant) Raitel-Not I Raitel-Pco RI Male. lat strand cDM was primed with a Not I - oligo(dT) primer downwaste of the control of the c

REFERENCE AUTHORS ORGANISM Notes aplene

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Dikaryota: Netazoa: Eumetazoa: Bilateria: Cocalomata:

Delterbertenia: Chocata: Pertebolata: Gathostomata: Osteichthyes:

Delterbertenia: Chocata: Terrepolata:

Sarcopterygii; Chocata: Terrepolata: Maniota: Marmalia: Theria:

Sarcopterygii; Chocata: Terrepolata: Maniota: Marmalia: Theria:

Delteria: Archonta: Primates; Catarrinia: Moninidae: Nomo.

Chases I to 474)

Hilleria: Clark, M. Dubuque, T. Eliston, K. Hawkins, M.,

Hilleria: Clark, M., Nicoba, T., Le, M., Lennon, G., Marra, M.,

Bolman, M., Millana, M., Riccha, T., Le, M., Lennon, G., Marra, M.,

Bolman, M., Millana, M., Riccha, T., So, Ar., Wohldmann, P. and

Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and

Wilson,R. The WashU-Merck EST Project Unpublished (1995)

Rabb: Merch ENT Project
Weshington Ditwrsity School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 326 180
Pax: 314 286 1810
Pax: 314 286 1810
Enail: serventson.wustl.edu
High quality sequence stops: 340
Source: IMAGE Consortium, LINU
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
Location/Qualificre
1. 1474

FEATURES Source

/organism="Homo sapiens" /clone="268069" <1. .>474 a 128 c 124 g 11

BASE COUNT ORIGIN 106 124 g 111 t

Query Match 3.9%; Best Local Similarity 100.0%; Matches 18; Conservative

Score 18; DB 19; Le Pred. No. 1.05e-04; 0; Mismatches 0;

Length 474 indels

0

Gaps

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Length 495;

Indels

0

Query Match 3.9%; Best Local Similarity 100.0%; Matches 18; Conservative Score 18; DB 10; Le Pred. No. 1.05e-04; 0; Mismatches 0;

ACCESSION AAS4144

9228768

KEYNORDS

ETT 9

SOURCE

ORGANISH

LONG-polia melanogaster

Discreption by tetaco, Arthropoda: Trachesta: Hexapoda; Insecta; Pregrence by tetaco, Enterprese broophila Droophila D RESULT 35
LOCUS
DEFINITION ANS41204 SO4 bp mRNA EST 12-7AN-1998 LD21043.5prime LD Drespphia melanogaster ambryo BlueScriptus Drespphia melanogaster ambryo BlueScriptus ANS41204 ANS41204 EST. 221043 Sprime, mRNA sequence. 221043 Sprime ambra sequence.

Contact: Barvey, G. School Biology University of California Berkeley (CA 94720-3200, USA Barkeley, CA Place State of the Total Control of Total California Control of the California Plate: 210 row: D column: 7 High quality sequence stop: 362

800 Apr 19 13:23:57 1999

US-08-836-455-3.rst

Email: estewateon vustl.edu
This clone is available royalty-free through LEML: contact the
TMAGE Consortium (infostange libilgov) for further information.
Possible reversed clone sailatrity on trong strand
seq primer: -40ml3 fwd. ET from Amersham
Location/Qualifiers
100ml3 fwd. ET from Amersham
Location/Qualifiers

Organisms "Rome applens"
//organisms "Rome apple

ib="Soares fetal liver spleen lNPLS S1"

/db\_xre="cpsi:199024'
/db\_xre="taxon:9600'
/clone='43268'
/clone='43268'
/de=\_Enger='plus (ampicillin resistant)'
126 a 113 c 113 g 131 t

Length 508;

BASE COUNT ORIGIN

Cuery Match 9, 198; Score 18: DB 12; Length 508 Best Local Similarity 100.0%; Peed No. 105s-04; Matches 18: Conservative 0; Hismatches 0: Indels

438 ACATCTTCACTGAGGCCC 455

DEFINITION
ACCESSION
NID
REYWORDS
SOURCE N40557 512 bp. 1 N4 yy48902.sl Homo sapiens ( N40557 91164154 EST. mRNA EST CDNA clone 276818 3'. 22-JAN-1996

Page 63

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US-08-836-455-3.rat

double-stranded cDNA was size selected, ligated to Zoo RI adapters (Pharmacia), dispated with Not I and closed state the Not I and Eco RI sites of a modified p777 vector (Pharmacia), Library went through one round of normalisation to a Cot = 5. Library was constructed by Bento Soares and M.Fatian Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (MINDS/NIN).

Dr. Kevin G. Becker (MINDS/NIN).

Dr. Kevin G. Decker (MINDS/NIN).

Eukaryoles: Metaros: Eumetaros: Bilateria; Coelomata:
Deuterostemia; Chordata; Verrebrata; Gostobatosconata; Osteichthyes:
Sarcopterygii; Choanta; Petrapod; Jamiote; Mammalla; Theria;
Eutheria; Archonta; Primates; Ceterphin; Moninidae; Mono;
I (bases 1 to 513)
Hiller; L. Clark, M., Dibuque; T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kuchba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Ritkin, L., Rohiting, T., Soares, M., Tan, F.,
Trevankis, E., Waterston, R., Williamson, A., Wohldmann, P. and

REFERENCE AUTHORS

Wilson,R. The WashU-Merck EST Project Unpublished (1995)

Reshir-Serok EST Project

Washington University School of Medicine

444 Pores Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810

Pax: 314 286 1810

Pax: 314 286 1810

Pax: 314 286 1810

Exact: a sequence stops: 420

Source: IMAGE Consortium, LIME

This clone is available royalty-free through LLML: contact the
IMAGE Consortium (IMAGE Consortium) CLML

Location (Vauliflers

Location (Vauliflers)

/organisme\*Homo sapiens\* /clone\*\*276818\* <1...>512 126 a 128 c 131 g 12 131 g 125 t 2 others

MRNA BASE COUNT ORIGIN

FEATURES source

Query Match Best Local s Matches 1 h 3.9%; Score 18; DB 19; Le Similarity 100.0%; Pred. No. 1.05e-04; 18; Conservative 0; Mismatches 0; Length 512; 0

Gaps

ğ 439 ACATCTTCACTGAGGCCC 456

AI138558 529 bp BRN

EST

23-SEP-1998

RESULT LOCUS

38

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Page 62

Location/Qualifiers

1. Sud
Organisma Drosophila melanogaster
//Organisma Drosophila melanogaster
//Organisma Drosophila melanogaster
//Organisma Drosophila melanogaster
Book; Steal; Xhol; Constructed using Strategene Zab-coba
Synthesis kit. Oilgo dr.primed and directionally cloned at
Ecost and Mhol; in BlueScript St(\*/-);
//Ab\_xref="BDGP\_EST:BDG1020070"
//Ab\_xref="Axxon"/272"
//Ab\_xref="Axxon"/272"
//Ab\_xref="Axxon"/272"
//Ab\_bost="Sold"
//Ab\_bost="Sold"
//Ab\_bost="Sold"
//Ab\_bost="Sold"
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//Ab\_bost="Sold"
//Ab\_Jost="Sold"
//Ab\_Jost

127 a

BASE COUNT ORIGIN

Query Match Best Local S Matches 1 36 TITCCAGGAAAAATATTT 53 !!!!!!!!!!!!!!!!!! 221 TITCCAGGAAAAATATTT 204 h Similarity 100.0%; 18; Conservative Score 18; DB 12; Length 504; Pred. No. 1.05e-04; 0; Mismatches 0; Indels 0;

> Gaps 0

RESULT 36 LOCUS AA779221 DEFINITION E339e03.8 221 508 bp mRNA EST 05-PEB-1998
03.81 Sources fetal liver spleen 1NFLS S1 Homo sapiens cDNA
452668 3' similar to TR:008810 008810 U5-116KD. ;, mRNA

KEYWORDS SOURCE ORGANISM ACCESSION AA779221 92838552 EST.

REFERENCE AUTHORS

DivaryCia: Metacos: Chordata: Vertebrata: Mammalia: Eutheria: Frimates: Catarthini; Hominidae: Homo. (Nese: 1 0508)

Hilles: 1 0508)

Hilles: 1 0508; Bowles: L. Debuque, T. Geisel, G., Jost, S., Rites, M., Evises, L., Debuque, T., Geisel, G., Jost, S., Rites, T., Lagy, M., Lennon, G., Marta, M., Hartini, J., Woore, B. Schellanberg, K., Steptoe, M., Tän, F., Thisiain, B., Malte, Y., Wylis, T., Waterston, R. and Milson, R. Washowit human Ess Project

Washowit human ess Project

Unpublished (1997)

Contact: Wilson RK.
Mashington Ontwrestty School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MD 63108
741: 314 286 1800
Fax: 314 286 1810

Apr
19
13:23:5
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REFERENCE AUTHORS TITLE

Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 450. Location/Qualifiers

KEYWORDS SOURCE ORGANISM

ACCESSION NID DEFINITION

Page 65

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Page 66

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AA610416 676 bp mRNA EST. 20-OCT-1997
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Frimates; Catarrinis; Reminidae; Hono.

1 (bases 1 to 529)
MCI-CAMP http://www.nebi.nlm.nih.gov/nciegap.
Mational Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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3' similar to TR:008810 008810 US-116KD. ;, mRNA sequence.
3544830 EST.
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Washington Onleraity School of Medicine ...

444 Forest Bark Parkway, Box 8501, St. Louis, MO 63108

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Tel: (301) 495-150

mail: Robert_Straubberghih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Patina
Bonaldo, Ph.D.
cDNA Library Prayed by: Grey Lennon, Ph.D.
cDNA Library Prayed by: Grey Lennon, Ph.D.
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Abbare fetaxon: 9806

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                                                             ACCESSION AADDAY.

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ORGANISH Home Anglens

Eukaryotan Parlantes: Catarrhini; Hominidae; Home.

REFERENCE 1 (bases 1 to 690)

AUTHORS KCI-CALP http://www.nobi.nlm.nih.gov/noicgap.

TITLE Mational Canner Institute, Canner Genome Anatomy Project Tumor Gene Index

JORRAL Unpublished (1997)

"obert Strausberg, Ph.D.

Michar
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Washington Star Priject
A444 Rotsett Park Parky Box 8501, St. Louis, MO 63108
Tel: 314 266 1800
Fax: 314 266 1800
Email: est@waseon.wust.edu
Email: est@waseon.wust.edu
This clone is available royelty-free through LiNL; contact the
INAGE Consortium (info@inage.linl.gov) for further information.
Insert Length: 741 is Gd Error: 0.00
Seg primer: mob.REGA-FT
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Location/Qualifiers
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Seq primer: -40ml3 fwd Er from Amersham
High quality sequence stop: 443.
Location/Qualifiers
1. 678
                                           Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: L. Jeffrey Medeiros,
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Query Match

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Unpublished (1997)

Project (CGAP)

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RESULT 40 LOCUS DEFINITION

Query Match 3.9%; Best Local Similarity 100.0%; Matches 18; Conservative

128

1 (bases 1 to 718) Riller, L. Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krisman, D., Knobb, T., Lacy, K., Le, N., Lennon, G., Harta, H., Martin, J., Moore, B., Schallanbery, K., Steptoe, H., Tan, F., Theising, B., White, Y., Waterston, R. and Wilson, R., Washd-WCI human Est Y., Wylde, T., Waterston, R. and Wilson, R., Unpublished (1997)

444 Forest Park Parkway, Box 8501, St. Louis, Tel. 314 286 1810
Fax. 314 286 1810
Fax. 314 286 1810

MO 63108

Email: estwateon, wasil.edu
This clone is available royalty-free through LAN, contact the
TRAGE Consortium (infodimage lin) gov) for further information.
Possible reversed clone; shallarity on wrong straid
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1. 738

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Indels 0;

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Clemson University Genomics Institute
Clemson University, Clemson University, Clemson, 5C
Tel: 864 656 4293
Pax: 864 656 4293
Danii: rdean@clemson.edu
Seq prime: GGNANCACTATCACCATC
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                                                                              CDMA Library Arraying: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MCT-CASP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLMU, at:

www-bio-llnl.gov/bbrp/image/image.html
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CDNA Library Preparation: Stratagene, Inc., David B. Krizman,
Ph.D.
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Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata;
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DEFINITION ACCESSION NID Best Local Similarity 100.0%; Matches 18; Conservative Contact: Robert Strausberg, Ph.D.
Tel: (201) 196-1550
mail: Robert Strausbergetih pov
This clone is available royalty-free through LLML; contact the
IMAGE Connorttium (infosimage.llnl.gov) for further information.
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The WashU-Merck EST Project
Unpublished (1995)
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Hiller, L. C. 209)
Hiller, L. C. 200; Marte, Dibuque; T. E. H., Lenon, G., Marte, H., Parsons, J., Ritkin, L., Rohling, T., Soares, M., Tan, F., Parsons, J., Ritkin, L., Rohling, T., Soares, M., Tan, F., Tervaskis, E., Materston, R., Williamson, A., Wohldmann, P. and Wilson, R., Waterston, R., Williamson, A., Wohldmann, P. and
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WashU-Merck EST Project
Washington University School of Medicine
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SOURCE Inhan primerwil Reverse library=Human White blood cells.

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REMARYSTEE HELECOM: Elmetaron: Bilateria: Coelomata:
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Barcoprerygil; Choanata: Tetrapoda: Amilota: Mammalia: Theria:
REPERENCE 1 (Dases 1009)

AUTHORS 1009; A.R., Fleischmann,R.D., Fuldner,R.A.,
Bulle,C.J., Lee,M., Mirhoss, E.F., Weinstook, G., Goosyne,J.D.,
White, D., Sariasaya,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bulle,C.J., Lee,M., Mirhoss, E.F., Weinstook, G., Goosyne,J.D.,
White,D.S., Sutton,G., Blade,J.M., Britchman, C., Chiu,M., Theria:
Bulle,C.J., Lee,M., Mirhoss, E.F., Weinstook, G., Goosyne,J.D.,
White,D., Sutton,G., Blade,J.M., Enrichman, C., Chiu,M., Theria:
Coeloman,J.M., McLine,R.T., Cotton, M.D., Enrich, M., M., Chilate, C.J., M., Britchman, C., Chiu,M., Stander, D., Chiu,M., Stander, D., Chiu,M., Chilate, C.J., M., Britchman, C., Chiu,M., Stander, D., Chiu,M., Chilate, C.J., Martin, C., Chiu,M., Chilate, C.J., M., Chilate, C.J., Chilate, C.J., Chilate, C.J., Mire, W., Chilate, C.J., Ch Query Match 3.7%; Score 17; DB 16; Length 209
Best Local Similarity 100 0%; Pred. No. 4.34e-03;
Matches 17; Conservative 0; Mismatches 0; Indels 70939 209 bp. nRNA. 5 end similar to immunoglobulin nu heavy chain, VDJ regions (GB:M17751) (HT:3055). 72838 951105 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 114 286 5810
Email: estematon.vustl.edu
Email: estematon.vustl.edu
High quality sequence stops: 110
Source: IMACE Consortium, LLNL
ITAGE Consortium (infosimange.llnl.gov) for further information.
Location/Qualifiers
1. 209 ô /organism="Homo sapiens" /clone="162881" a 66 c 56 g 41 t 6 others ..

US-08-836-455-3.rst

Pitterand L.M., FittBugh, M.M., Fritchman, J.L., Geoghagen, N.S. M., Glodek, A., Gonbin, C.L., Ranna, M.C., Hedblone, H.B.Dia JT.P.S., Kelley, J.C., Liu, L.T., Marmaros, M., Merrick, J.M., Mozeno-Palanques, R.F., McDonadd, L.A., 19yen, D.T., Pelleyinn, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shilay, R., Small, R.V., Spriges, T.A., Uterback, T.R., Weldman, J.F., Li, Y., Bedmarik, D.P., Cao, L., Cepeda, M.A., Collins, E.J., Dinke, D., Fenge, T.A., Cheene, J.M., Li, H., Collens, T.A., Collins, E.J., Dinke, D., Fenge, P., Ferrick, C., Bastings, G.A., He, N.-W., Bu, J.-S., Geene, J.M., Li, H., Griber, J., Radeon, P., Kina, A., Konak, D.L., Kansch, C.J., M., Li, H., Gerber, J., Ruden, J.R., Kina, M., Charles, J., Stancon, R.R., Rosen, C.A., Li, H., Marsell, C., Stater, M.A., and Venter, J.C., Martings, G.A., Stater, J.M., and Venter, J.C., Li, H., Marsell, C., Ming, J., Martings, M., Marsell, C., Ma

Contact: Venter, 30
The Institute for Genomic Research
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/organism="Romo sapiens"
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Query Match 3.7%; Best Local Similarity 100.0%; Matches 17; Conservative Score 17; DB 16; Length 238; Pred. No. 4.34e-03; 0; Mismatches 0; Indels 0;

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AA48804 159 pb mRNM SET 11-AUG-1997
ablid07:r1 Strategene lung (#937210) Homo saptens CDNA cloure #40613
5° similar to gb:855735 IG ALPHA-1 CHAIN C REGION (HUMAN);; mRNA
sequence.
AA488043
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ORGANISM

REFERENCE AUTHORS

Page 78

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REFORDS 509707

KETWORDS 525.

SOURCE human primerwill Reverse library-Human Pancreas.

DIGANTSH Human primerwill Reverse intracy, Bilateria, Coclomata, Bidaryothen, Metazoa, Bilateria, Coclomata, Chocata, Choc
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METMODIS 257.

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Hillser,L., Alten M., Bowles,L., Dubuque,T., Gersel,G., Jost,S.,
Kucaba,T., Lery,M., Ler,N., Lennon,G., Narra,M., Martin,J.,
Moore,B., Schollanberg,K., Stephoe,H., Tan,F., Theising,B.,
White,T., Wyle,T. project property of the control of the
Washdrerck Ear Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RY.
Washington University School of Medicine
4444 Forest Rarversity School of Medicine
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7441 214 286 287
Fax: 114 286 2880
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Eukaryotae; mitochondrial eukaryotes: Metazoa: Chordata;
Vortebrata; Kammalia; Eutheria; Primates; Catarrhini; Hominidae;
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The Institute for Genomic Research
323 Clopper Rd, Gaitheraburg, ND 20078
724. 301899056
Fax: 301899056
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12 Medical Center Drive, Rockville, MD 20850
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/clone\_lib="Testis tumor"
/sex="malle"
/dev\_stage="adult"
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63 a 74 c 85 g 56

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Gaps

RESULT 49
LOCUS AA300571 279 bp mRNA
DEFINITION EST13661 Testis tumor Homo sapiens cDNA

BASE COUNT ORIGIN

71 g

Query Match
Best Local Similarity 100.0%;
Matches 17; Conservative

FEATURES Source

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GENESEQP: R21279
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(Peptide) WORDSEARCH of: /home/obryen/ree455/olig/us-08-836-455-4 check: 265 from:
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## Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U Distribution rights by Oxford Molecular Ltd Unit.

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Title: Description: Perfect Score: Sequence: >US-08-836-455-4 (1-153) from US08836455. 153 MECSWVFLFLLSITTGVHSQ. pep

Scoring table: Gap 60 unitprotable

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### Numanised heavy chain 6.52e-00 ### S.2 14210 ### S189	Non Apr 19 13:23:58 1999 US-08-836-455-4.rag	## Reshaped human AVX12	Mon Apr 19 13123158 1999 US-08-836-455-4.rag

### Anti-CEA antibody hea 5.39e+01   ### Anti-CEA antibody heavy chain 5.39e+01   ### Anti-CEA antibod 5.39e+01   ###	Mon Apr 19 13:23:58 1999 US-08-836-455-4.rag	### S.2 475 12 Wilsy ### Wilsy ### S.2 1211 DR R2529 Sequence of GEVET. ### S.2 1221 DR R2529 Heavy chair curvalele 5.52e-00 ### S.2 1221 DR R2529 Heavy chair curvalele 5.32e-01 ### S.2 1221 DR R2529 Heavy chair CRR2 of C 5.33e-01 ### S.2 1221 DR R2529 Heavy chair CRR2 of C 5.33e-01 ### S.2 1221 DR R2529 Heavy chair CRR2 of C 5.33e-01 ### S.2 1221 DR R2529 Heavy chair CRR2 of C 5.33e-01 ### S.2 1221 DR R2529 DR R252 DR R252 DR R252 DR R252 ### S.2 1221 DR R2529 DR R252 DR R252 DR R252 DR R252 ### S.2 1221 DR R2529 DR R252 DR	Mon Apr 19 13:23:58 1999 US-08-836-435-4.rag
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RESULT 7 ID R33345

standard;

Protein; 134

8 B

127

standard;

Query Match Best Local S Matches 1

e 134 AA; h 12.4%; Similarity 100.0%; 19; Conservative

Score 19; DB 6; Pred. No. 1.38e-11 0; Mismatches

Length 134;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apr 19 13:23:58 1999
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Best Local Similarity 100.0%;
Matches 19; Conservative
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06-ULT-1993 (first entry)
06-ULT-1993 (first entry)
Sequence of the variable region of the heavy chain of
monoclonal antibody; NM-O1; HIV-1; gpl20; gp160.
Synthetic.
W0304099A.
W0304099A.
W04-MA-1993; U07111.
24-MC-1992; U07111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hatical rinombhyonic anties obligate antibodies - for diagnosis and thrapy of accidence -g breast or colorectal carciness of thrapy of accidence -g breast or colorectal carciness (Claim 14: Page S3: 67pp; English.

071395 codes for 860565 the antibody heavy chain region of murine-human anti-carcinembryonic antigon (CEA) chimeric antibody. Which can be used in a vitro immunosasys for the detection of CEA, and monitoring of tumour-associated antigen during therapy. It can also be used in vivo diagnostically, or in therapy for the treatment of tumours associated with colorectal and breast carcinomas, as well those of the sattonices in a well those of the sattonices in the sattonices in a second colorectal and breast carcinomas, as well those of the sequence 114 Ab;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BB, Kaplan DA, Mezea PS, -294331/36.
Q71396.
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Pred.
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. No. 1.38e-11;
Mismatches 0; Indels
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complementarity determining

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PR 18-DAN-1988; US-942019.

PR 18-DE-1992; US-98755.

PR 18-NUC-1984; US-998055.

PR 28-AUC-1984; US-998055.

PR 28-AUC-1984; US-998055.

PR 29-AUC-1984; US-998055.

PR 29-AUC-1986; US-998055.

PR 2
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AC R7
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PR 22-AUG-1991 08-40552.

PR 22-AUG-1991 08-407311.

PR 22-APR-1993 US-1039457.

PR 24-AUG-1993 US-1039457.

PR 4991 96-44236744.

PR 4991 96-4423674.

PR 4991 9
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Best Local Similarity 100.0%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                       LT 9
R74961 standard; Protein; 135 AA.
R74961; PS (first entry)
Anti-Idlotype antibody Idio17 clone 17cB7.
Antibody; cancer; anti-Idiotype; CDR: heavy
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                                                                                                                                        "-MAR.1997 (first entry)
nocional anticky MY-01 heavy chain variable region coding sequence
nocional anticky virus type-1; HIV-1; spl20; spl10; spl10; sp.
nocional anticky; infection; heavy chain; light chain; hybridoma,
no_saplens.
                                                                                                                                                                                                                         h 12.4%;
Similarity 100.0%;
19; Conservative
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d. No. 1.38e-11;
Mismatches 0;
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. No. 1.38e-11;
Mismatches 0; Indels
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PH US5598417-A.

1 Abel- mat_peptide

PH 15 - DE-1997.

1 G-7DH-1995. 466203.

PH 2 - MA-1995. US-501092.

PH 2 - MA-1995. US-50731.

PH 3 - MA-1995. US-50731.

PH 4 - MA-1995. US-50731.

PH 3 - MA-1995. US-50731.

PH 4 - MA-1995. US-50731.

PH 5 - MA-1995. US-50731.

PH 6 - MA-1995. US-50731.

PH 7 - MA-1 - MA-1 - MA-1995.

PH 1 - MA-1995. US-50731.

PH 5 - MA-1995. US-50731.

PH 6 - MA-1995. US-50731.

PH 7 - MA-1 - MA-1995. US-50731.

PH 1 - MA-1 - MA-1995.

PH 1 - MA-1 - MA-1995.

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Best Local S
Matches 1
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Peptide
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Mouse 2N7 antibody heavy chain variable region.

Mouse; murine; heavy chain variable region;

Mouse; murine; heavy chain; variable region;

munosplobulin fragment production; ig fragment production;

monoclonal antibody 2N7, human B-cell surface antigen.

Mus sp.

Torottin/muliface.
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s sp.
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Similarity 100.0%;
19; Conservative
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1..19
/label= sig_peptide
20..140
/label= mat_peptide
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32

RESULT 11 ID W47520 standard; Protein; 140 AC W47520;

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specific ly chains in various organisms provides an effective solution for the efficient large scale production of human monoclonal antibodies. The invention also provides a solution the problem of class switching antibody molecules. Sequence, 140 Ak;

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Page 33

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Gaps

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Page 34
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PR 03518920-A.

PR 01-NRY 185: 793980.

PR 01-NRY 185: 08-793980.

PR 01-NRY 185: 08-79398.

PR 11-ANH 1888: 08-112039.

PR 11-ANH 1988: 08-112039.

PR 11-ANH 1992: 08-870404.

PR 12-ARR 1994: 08-870404.

PR 13-ARR 1994: 08-970404.

PR 13-ARR 1994: 08-9704.

PR 13-ARR 1994: 08-
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W47513 a
W47513;
05-JUN-;
Mouse;
Mouse;
Mouse;
Monoclor
Mus sp.
Key
Peptide
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287 anthody heavy obain variable region,
marine; heavy chain variable region;
oglobulin fragent production; 3g fregent production;
onal antibody 287; human B-cell surface antigen.
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Similarity 100.0%; I
19; Conservative i;
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Similarity 100.0%;
19; Conservative
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69.85
/label= CDR2
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86.117
86.117
118.130
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1.19
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131. 136-1= FR4
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Score 19; DB 23; LA
Pred. No. 1.38e-11;
; O; Mismatches O;
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Pred. No. 1.38e-11;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                     Length 140;
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                                                                                      PH US5595988-A.

PH US5595988-A.

D1 11-JAN-1997.

PH O1-Nov-1995 79380.

PH O2-HAR-1990 US-901092.

PH O3-HAR-1990 US-901092.

PH U3-HAR-1990 US-901092.

PH U3-HAR-1990 US-901092.

PH U3-HAR-1990 US-901092.

PH U3-HAR-1990 US-901093.

PH U3-HAR-1990 US-9000 US-90003.

PH U3-HAR-1990 US-90003.

PH U3-HAR-1990 US-90003.

PH U3-HAR-1990 US-90003
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M10588 sandard: Protein: 140 AA.
M10589: 21-007-1997 (first entry): sandard: region.
21-007-1997 (first entry): sandard: recombinant production: municopiobilio (; IgG; heavy chain: recombinant production: municopiobilio (; IgG); heavy chain: recombinant production: fimuncosasy: langing: regient; complement neddated lysis: fimuncosasy: variable; region: complementarity determining: CDR: framework.
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Jobel CDR1
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118.130
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Page 38

TYGE-) Int Genetic Eng Inc.

Disson RR, Liu AX, Horvitt AH, Wall R, Better M;

PI: 89-061144/08.

PSDB: 1891146.

Solynucleotide(s) encoding Immunoglobulin molecules.

sed for efficient prodn of chimeric human or non-human or lass switched antibodies.

lass switched antibodies are useful in passive immunoglobulin equence carries the variable region of the chimeric immunoglobulin equence. The antibodies are useful in passive immunisation avoiding espative immune reactions. They are also useful in assaying and in vitro median.

98; 02514. 97; US-077528. Tr Genetic Eng Inc. RR, Liu AY, Horwitz AH, 1 11144/08.

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cc molecule comprises 2 DNA sequences encoding 2 pectate lyase caretion signal sequences respectively linked to a DNA sequence can strong and 15 rd molecule or 19 light chain, operably linked to a control of the cont
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Query Match 12.4%;
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Matches 19; Conservative
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p94780 standard; prv...
P94780 (first entry)
06-UUL-1990 (first entry)
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07-MAR-1987;
27-CCT-1965; U02269;
01-W0Y-1965; US-793980.
(1702-) HT GENETIC ENG INC.
(ROBL/) ROISINSON R R.
Robinson RR. Liu AY, Horwitz AH, Wall R:
WFI: 87-11500//19.
Prodn. of immunoglobulin chains and molecule
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/*tag= g

12abel=CDR3

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RESULT 17

ID #10242 standard; Protein; 140 AA.

D #10242;

MC #10242;

DT 06.MG-1997 (first entry)

DZ Heavy chain variable sequence of 2H7.

RW Pectate lyass; signal sequence; Gram-negative bacterium; immunoglobulin;

RW protein production; human; constant region; passive immunisation; toxin;
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//tabel=PR1
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/label=leader
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antibody; Ig; heavy-chain; hepatitis; mouse; lung carcinoma; cancer;
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Mus musculus.
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visys standard; Protein: 159 AA.
visys; standard; Protein: 159 AA.
visys; standard; protein: 159 AA.
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/note "framework region 1"
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118..133
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134..144
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PH D4-D2C-1996.

PH D4
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PR 14 MR-1995; 197551.

PR 15 MR-1995; 197551.

PR 15 MR-1995; 197551.

PR 15 MR-1995; 197551.

PR 15 MR-1995; 197551.

PR 16 MR-1995; 197551.

PR 16 MR-1995; 197551.

PR 17 MR-199551.

PR 17 MR-199561.

PR 17 MR-199551.

PR 17 MR
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RESULT 25

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BY 305629446-A

Sequence present sequence represents the variable region of the heavy antibody 7612, produced by the hybridoms ZMA7612.

uence 212 AM; chain

**장** B Query Match 12.4%; Best Local Similarity 100.0%; Matches 19; Conservative 96 dywgggtavtvasakttpp 114 ||||||||||||||||| |125 DYWGQGTSVTVSSAKTTPP 143 Score 19: DB 24: Length 212; Pred. No. 1.38e-11; 0: Mismatches 0: Indels 0;

Gaps

0

RESULT
ID WI
AC WI
DI OS
DE AI
OS ME
PN WI
PD 2 77 24
W15914 sandard: Protein: 222 AA.
W15914 sandard: Protein: 222 AA.
W15914
09-DEC-1997 (first entry)
Antibody 302 heavy chain variable region.
catalytic antibody: enantioselective hydrolysis:
AA.0012: ZAA.002: da.
kma 125 hybridoma;

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19 13:23:58 1999
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pr 17-MAR-1995; J00462.

pr 17-MAR-1995; WO-JD0462.

pr 18-MAR-1995; J0462.

pr 18-MAR-1995; J0462.

pr 18-MAR-1995; J0462.

pr 18-MAR-1995; J0462.

pr 18-MAR-1996; J0472.

pr 18-MAR-1997; J0472.

pr 18-MAR-1998; J0472.

pr 18-MAR

of antibo present sequence represents the variable region of antibody 362, produced by the hybridoma ZAA3G2. the heavy chain

5 B

Query Match Best Local S Matches 1

h 12.4%; Similarity 100.0%; 19; Conservative

Score 19; DB 24; Le Pred. No. 1.38e-11; 0; Mismatches 0;

Length 222;

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Caps

standard; Protein; 230

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997 (first entry)
nocional antibody B9 heavy
asma apolipoprotein B-100; chain. arteriosclerotic lipoprotein;

ID W37088 standars
AC W37088 standars
AC W37088.
DT 18-NOV-1997 ()
DE House monoclone
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31.35
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Best Local Similarity 100.0%; Matches 19; Conservative Pred. Indels 0 Gaps

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22
7306 standard; peptide; 170 AA.
7906; etandard; peptide; 170 AA.
7907-1999; (first entry)
use monoclonal entibody 1608 heavy chain sequence derived
NA. anised antibody; TM29; T cell; Crohn's disease

on Synthetic machody; 1823; Totali, Crohn's disease.

PN 40051603; 40087.

PD 15-70W-1995; 80-025183.

PF 21-80V-1994; 180387.

PR 08-DOZ-1993; 60-025183.

PA (PEEC) MERCER C. P.

PE (PEEC) MERCER C. P.

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re 19; DB 13; Ler d. No. 1.38e-11; Mismatches 0; Length 170; L1; 0; Indels

g Query Match 12.4%; Score Best Local Similarity 100.0%; Pred. Matches 19; Conservative 0; M 162

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RESULT 23 ID W15932 standard; Protein; 212

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Prof. 1991; 200767

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Synthetic.
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RR1687 standard: Protein; 235 AA.
RR1687 standard: Protein; 235 AA.
RR1687 standard: Protein; 235 AA.
V1-Lab-Vh construction (4A), single chain entibody.
V1-Lab-Vh construction (4A), single chain entibody.
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9-MAY-1995; RR-039459.

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FP1 97-86706//44.

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9-95DB: T85090.
Location/Qualifiers
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R14684 sandard: Protein: 235 AA.
R14684 sandard: Protein: 235 AA.
R14684
V)-I-Mab-1992 (first entry)
V)-Lab-Vh construction (JA), single chain
ScA: ScAN; trombus; t-PA; urokinase.
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/note= "mutation
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||||||||||||||||||||
125 DYWGGGTSVTVSSAKTTPP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
onstruction (3A), single chain
trombus; t-PA; urokinase.
                    Location/Qualifiers
1.108
/label= V1
/note= "from MA-15C5"
109.115
109.15
116.235
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/notes "from NA-1505"
100: 115
/Aabai Lab
115: 215
/Aabai VN
/Notes "from NA-1505"
/Aabai Vl_anchor_region
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1..108
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Pred. No. 1.38e-11
0; Mismatches
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Pred. No. 1.38e-11;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody
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Query Match 12.4%; Best Local Similarity 100.0%; Matches 19; Conservative

26 R14695 sta. C R14695; O1-FEB-1992 / V1-Lab-Vh r V1-SC#

standard; Protein; 235 AA

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Apr 19 13:23:58 1999
/label vh
/note "rom MA-1505'
100.104
/label vl_anchor_region
118.122
/label vl_anchor_region
00 /label vl_anchor_region
00 /label vl_anchor_region
00 /label vl_anchor_region
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/note= "mutation w.r.t. original sequence"
108
/note= "mutation w.r.t. original sequence"

//note \*trom MA-15C5\*
//abol= Lab
1/1.216
1/1.216
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Whoshidassa. //noce\* mutation w.r.t. original sequence\*
by 1007-1991.
pp 11-007-1991.
pp 11-00

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RESULT
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                                                                                   II 30
R15590 standard; Protein; 236 AA.
R15590;
R15590;
Ul-Fab-1992 (first entry)
Vl-Lab-Th construction (4A), single chain antibody
SCA; SCAPA, trombos; t-PA; urckinase.
Synthetic.
    Key
region
                                                misc_difference
                                                                 / Match 12.4%:
Local Similarity 100.0%;
les 19: Conservative
Location/Qualifiers
1.108
/label= V1
                                                                Score 19; DB 3; Len
Pred. No. 1.38e-11;
0; Mismatches 0;
                                                                         Length 235;
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py MODISISSA. /ROCE "NUTRILION W.F.t. Original sequence" pp 11077-3931.
pp 21.077-3931.
pp 31.077-3931.
pp 31.
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PR (COMYS, 1904; EP401090.

PR (C
Query Match 12.4%;
Best Local Similarity 100.0%;
Matches 19; Conservative
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Ol-PER-1992 (first entry)
VI-Lab-Th construction (4A), single chain
SCA, SCAPA; trombus; t-PA; urokinase.
Synthetic.
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/label= Wh_anchor_region
/note= 'mutation v.r.t. original sequence'
/note= 'mutation v.r.t. original sequence'
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/note= "mutation v.r.t. original sequence"
/note= "mutation v.r.t. original sequence"

/label= Vh\_anchor\_region

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RESULT 31
1D R15591 standard: Protein; 237 AA.
1D R15591; 97 01-FEB-1992 (first entry)
1D 01-FEB-1992 (first entry)
1D V1-Lab-Yn construction (AA), single c
KW SCA; SCAPA; trombus; t-PA; urokinase.

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Query Match Best Local S Matches 1

h 12.4%; Similarity 100.0%; 19; Conservative

Pred.

re 19; DB 3; 1. No. 1.38e-Mismatches

: DB 3: Leny 5: 1.38e-11; 5: 5-6 0;

Length 236;

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RESULT 32 ID R15692 standard; Protein; 238 AA.

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°, Length 238;

Indels

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Gaps

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Query Match 12.4%; Best Local Similarity 100.0%; Matches 19; Conservative

Score Pred.

re 19; DB 3; Lend. No. 1.38e-11; Mismatches 0;

Length 237,

0

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Howelds: More mutation w.r.t. original sequence.

Note: More 1991; 200767,

PR 13-NR.1991; 29-401990.

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PR 100NP Company Br. Manae
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R15533 standard: Protein: 239 An.
R15533 Control of the contro
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PP 29-NOV.1993; GO2510.

PR 03-UN-1994; GO-204819.

PR 03-UN-1994; GO-204819.

PR 03-UN-1994; GO-201899.

PR 103-UN-1994; GO-201899.

PR 103-U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JSULT 15

R7605;

R7605;

R7605;

AT 31-NOV-1995 (first entry)

DE NAD 5-1 heavy chain.

RW Antigen binding structure; complementarity determining region; CDR; RW Antigen binding structure; tumor-sasociated antigen; hybridoma; RW ACA5-1, colorectal cancer; tumor-sasociated antigen; hybridoma; RW monoclonal antibody; Mab; immunotherapy; therapy; diagnosis; RW transgenic animal; transgenic plant; antibody engineering; RW humanized antibody; immunotoxin.
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Best Local Similarity 100.0%;
Matches 19; Conservative
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Pred. No. 1.38e-11;
0: Mismatches 0;
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FINE WODINGSSA.

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RIA699; Olivert entry);
Oliver-1992 (first entry);
VI-Lab-Th construction ($A), etc.
SCA, SCAPA; trombus; t-PA; urok
Systhetic: | constanting |
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(first entry)
construction (5A), single chain antibody.
trombus; t-PA; urokinase.
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d. No. 1.38e-11;
Mismatches 0;
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BULT 18 standard; Protein; 448 AA.

1896613 standard; Protein; 448 AA.

1896613 standard; Protein; 448 AA.

1906013 standard; Protein; 448 AA.

100711996 (first entry)
Anti-boll monoclonal antibody shadin shiding molec heavy chain; light chain; monoclonal antibody; Mb;
bovine growth hormone; boll; jumunoaffinity purification.
                                                                                                                             re 19; DB 13; Lei
d. No. 1.38e-11;
Mismatches 0;
                                                                                                                                          Length 445;
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                                                    molecule;
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                                                                                                                                                                          Query Match
12.4%;
Best Local Similarity 100.0%;
Matches 19; Conservative
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pp 03-287-1398; 902971.

pp 03-287-1898; 902971.

pp 03-287-1898; 9029217.

pp 03-287-1898; 902-29217.

pp 03-387-1898; 902-29217.

pp 03-387-1898; 902-29217.

pp 03-387-1898; 902-29217.

pp 03-387-1898; 902-29217.

pp 03-387-1899; 902-29217.

pp 03-387-1899; 903-29217.

pp 03-387-1899; 903-29217.

pp 03-387-1899; 903-29217.

pp 1814 RE, Hardman K, Ladner RC;

pp 1815 Ladner Pales Inc.

pp 1815 Ladner Pales Inc.

pp 1815 Ladner Pales Inc.

pp 1815 Ladner RC;

pp 1815 Ladn

Pred. re 19: DB 18; Ler 1. No. 1.38e-11; Mismatches 0; Length 448; 0 Caps 0

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C 843673 eandard: Protein: 448 AA.

C 843673.

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E Nouse anti-boyle growth hormone MAD heavy chain.

W Monoclonal antibody: MAD: affinity: binding: antigen: di
therapy: imaging: purification: blosensors.

W March Construction.

W 052302030-A.

U 052302030-A.

U 052502030-B.

0 05-NOV-1993.

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**8** B

109 dywgggtertvssakttpp 127

Query Match Best Local S: Matches 19

12.4%; Similarity 100.0%; 19; Conservative

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                           ph wobsisses, // Property Co. Hall SM. Paterson DS;
PR 03-UNN-1994 GB 0.1461.9
PR 03-UNN-1994 GB 0.146
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ID 89276 standard: Protein; 448 AA.

KA 89276;

AC 89276;

BY WITHOUTH STATE 
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PR 13-NR-1969; US-929917.

PR 15-NR-1969; US-299917.

PR 25-NR-1969; US-1974.

PR 1971; S1-967875/46.

PR 1972; S1-967875/46.

PR 1
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Best Local Similarity 100.0%;
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[Prof. [COWRI-13]] "1-7-K-A-P-K-N-[RCVR(8-105)]-P-G-B-[LCVR(4-5-109)] and construction is designated TRY40 (see Q05710,R06478).

Sequence 448 AA)
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Mismatches 0; Indels
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Disclosure: Fig. 15; 121pp; English.

Abb 55:1 (ECACC 9308;901) recognises the colorectal tumor-associated
antigen CAS5:1. cDNAs for the heavy (094037) and light (094036)
chains of 55:1 were isolated, and f(ab); F(ab); Fab. Fv, scpv or
"min humanized 55:1 constructs have been expressed in myeloma
cells and B. coll.
Sequence (4d Ab);
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WPI; 96-259060/26
N-PSDB; T29056
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Pred. No. 1.38e-11;
O; Mismatches O; Indels
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d. No. 1.38e-11;
Mismatches 0;
                                                                                                                                                                                                    anti-virus antibody .
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immunogenic, easier
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Indels

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Page 65

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43 90837 standard; Protein; 90837;

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.JUN-1996 (first entry)
I single chain antibody from pCIB4631.
Ita endocoain; Becillus thuringiensis; vestern corn rootworm;
Ita endocoain; Becillus thuringiensis; vestern corn rootworm;
RR; maize; pesticide; brush border membrane vesicie; monoclonal;
\*\*ho-dv. US-08-836-455-4. rag

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Query Match
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Matches 1
                                                                                                                                                                               monoclonal antibody. The cDMAs were incorporated into a 7i plasmid vercor, which was incorporated into A. tumefacian. The resultant plasmic expression vertor was used to transform tobacco plants, making them TMV resistant, the plants out a also be biofarmed for the prodm. of anti-virus antibodies.
129 dywgggtsetvasakttpp 147
||||||||||||||||||
|125 DYWGGGTSETVSSAKTTPP 143
                                                                                  h 12.4%;
Similarity 100.0%;
19; Conservative
                                                                                      Score 19; DB 13; Length 465;
Pred. No. 1.38e-11;
O; Mismatches O; Indels
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standard: Protein: 466 AA 991 (first entry) ti-carcinoembryonic antigen chain. obulin; carcinoembryonic antigen chain.

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-Thi-1996
-TUR-1998; IE0407;
-TUR-1998; US-27641.
CIBA, CIBA GETY MAG.
ARCHI MB [Collect MG]
FD: 90-07749/08
AG.
H-9830 [1573]
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5 B Query Ma Best Loc Matches Match Local h 12.4%; Similarity 100.0%; 19; Conservative Pred. re 19; DB 4; Leng d. No. 1.38e-11; Mismatches 0; Length 466; Indels 0 Gaps 0

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                                                                    human milk fat globule:
Mus musculus.
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/label = CDR2
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99.107
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                                 - cDR1
complementarity
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sapecially breast cancer [17]
Example 2: Hig JGC; 10bpp; Edgilsh.

Example 2: Hig JGC; 10bpp; Edgilsh.

This polypeptide sequence comprises a consensus sequence of murine heavy chain variable regions[(H)] selected on the basis of identity to the WH region (see W27120) of monoclonal anti-diotype antibody 1DDIO. The sequences were obtained from a Genshank database season.

A VL consensus (W27121) was also produced. 1DIO has a titles 118 department (W27121) was also produced. 1DIO has to least 18 department (W27121) was also produced. 1DIO has to least 18 department (W27121) was also produced. 1DIO has to least 18 department (W27121) was also produced. 1DIO has to least 18 department (W27121) was also produced. 1DIO has to least 18 department of the consensus sequences (7 in the 119th Collaboration Collabo Sequence 118 AA;

Query M Best Lo Matches Match 11.8%; Score Local Similarity 85.7%; Pred. es 18; Conservative .:0; N re 18: DB 25: 1. No. 1.86e-: Mismatches DB 25; L. 1.86e-10; Length 118; Indels 0 Gaps

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RESULT 4

ID #27122 standard: Protein: 118 AA.

AC #27122:
DT 04-JAN-1998 (first entry)
DE Murine antibody heavy chain variable region consensus.

EW Honoclonal antibody 11D10: anti-idiotype antibody: mucin:

ð ĝ

279 143

Query Match 12.4%; Best Local Similarity 100.0%; Matches 19; Conservative

Score Pred.

re 19; DB 16; Len d. No. 1.38e-11; Mismatches 0;

Length 599;

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Sequence

Page 6

77 45
R48513 standard: Protein: 134 AA.
R48513:
03:82P-1994 (first entry)
8-equence of the monoclonal antibody RM-01 heavy chain
variable regions.
Ruman immunodeficiency virus: RIV-1 AIDS; glycoprotein: V3 loop;
gp120: epitope: monoclonal antibody: RM-01: variable heavy.

-MAR-1994. -AUG-1993; U07967. -AUG-1993; W0-U07111. -APR-1993; US-039457. 475P) NISSIN SHOKUHIN E KAISHA

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WPI; 94-083117/10. N-PSDB; Q56685.

We ready, Visual Antibody specific for epitope on HIV-1 qp 120problem and the control of the passes immunisation to tract acid
proposition of the control 
Query Match 11.8%; Best Local Similarity 100.0%; Matches 18; Conservative Score Pred. re 18; DB 9; Lend. No. 1.86e-10; Mismatches 0; Length 134;

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110 ywgggtsvtvssakttpp 127 |||||||||||||||||| 126 YMGQGTSVTVSSAXTTPP 143

8 B

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Apr 19 13:23:58 1999
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70
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RESULT 40

W41391 standard: peptide: 34 AA.

W7 07-3731-390 (first entry)

W7 cancer dasgnoads: complementarity determining region; heavy chain.

W8 07-12329-AA.

PM 07-12329-AI.

PM 07-1239-1, 03-003103.

PM 14-PER-1997: 03-00310
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Matches 17; Conservative
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which binds to surface
human C regions avoids
Sequence 447 AA;
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A monoclonal antibody (Mab) which has donor CDR's of foreign origin
and a recipient framework of human or primate origin, where the
crisinal amino acid as position 29 or 78 of the heavy (N) chain of
the framework is replaced by an amino acid the same as or similar to
that in the corresponding position of the Hohin of the Ab from
which the CDR's are derived, can be used for the treatment of cancer,
and autoimume diseases, specifically multiple myeloms. Imphoma and
temmicold arthritis. The Mab binds to CDNs. Replacing framework
residues 39 and 80 of the humanised Ab with the original donor
residues are cores the antigen binding activity of the antibodies.
Sequence 11 Ai.
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R99941 standard: Protein: 151 AA.
R99941;
03-JAN-1997 (first entry)
Humanised anti-CD39 monoclonal antibody variable heavy chain.
Honoclonal antibody; Abb humanised: cancer: autoimmune disease:
multiple mysloms: lymphoms: rheumatoid arthritis; CD39;
homphementary determining region; CD8: heavy chain; light chain.
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UN 1566; Standard: Protein; 118 AA.

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Search completed: Thu Apr 15 18:13:33 Job time : 92 secs.

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PIR1: HVMS8A
PIR2: PH1005
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### STATES   STATES   Call receptor beta   15+02	Mon Apr 19 13:23:59 1999 US-08-836-455-4.rpr	### 1356   PH4412   Jy heavy chain v xeg   1.55e-00   ### 136   137   2.55e-00   ### 136   137   2.55e	Mon Apr 19 13:23:59 1999 US-08-836-455-4.xpx

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#molecule_type_DNA #residues 1-95 #label MOJ #crear-reference EMED:2244; MID:#407814; PID:#407815 CLASSIFICATION #apperfeatly munoglobulin V region; immunoglobulin homology EXTMORDS immunoglobulin Planting #comain immunoglobulin homology #label IAM #crear and the properties of the	RESULT 5  S42178 stype fragment FITTLE ORGANISM	###Dictoil=_type_DNA ###Dictoil=_type_DNA ###Dictoil=_type_DNA ###Dictoil=_type_DNA ###Dictoil=_type_DNA ###Dictoil=_type_DNA ###Dictoil=_type_DNA ###Dictoil=_type_Tanily_immunoglobulin v region: immunoglobulin homology ###Dictoil=_type_Tanily_immunoglobulin homology ###Dictoil=_type_Tanily_immunoglobulin homology ###Dictoil=_type_Tanily_immunoglobulin homology ####Dictoil=_type_Tanily_immunoglobulin homology ####Dictoil=_type_Tanily_immunoglobulin homology ####################################	Mon Apr 19 13:23:59 1999  OB-Sep-1997 ACCESSIONS 84217 REFERENCE 92176 Fournat Ed. J. Immunol. (1993) 23:2603-2510 Fournat Variable region gene extension of immunoglobulin G-expressing Collagen. For the Collagen.  Section 942:17  Section	***Creations***  ****Creations***  ****Creations***  ****Creations***  *****  *****  *****  *****  *****  ****	3000

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ACCESSIONS REFERENCE #Authors #journal

Mo, J.A.: Bone, C.A.; Holmdehl, R.
Eur. J. Kmwunol. (1993) 33:2503-2510
Variable region gene selection of immunoglobulin G-expressing
B cells with specificity for a defined epitope on type II
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S42181 stype fragment
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if ormal\_name Mus wasculus \*common\_name house mouse
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80.71A.; Bona, C.A.; Holmdahl, R.;
Eur. J. Immunol. (1993) 33:2503-2510
Variable region gene selection of immunoglobulin G-expressing
Paris with specificity for a defined epitope on type II
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Ig heavy chist precursor V region - mouse

# formal_name Kwa muscults # common_name house mouse

11_Dec_1993 # sequence_revision 31-Dec_1993 # text_change

08-Sep_1997

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Craft, P.J; Levin, S.D.; Gilbert, T.; Kindsvogel, W.

Mucleic Acida Res. (1997) 15:5496

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8 cornal_same Mus musculus *common_name house mouse
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6 gamma chim V region - mouse house mouse
6 cormal\_name Nws musculus frommon\_nemb house mouse
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1-102 #label NOJ
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19 gamma chin V region : mouse (fragment)

#formal\_name Mus musculus \*common\_name house mouse

#formal\_name Mus musculus \*common\_name house mouse

20 -Sep-1944 \*sequence\_revision 21-Jul-1995 \*text\_change

08-Sep-1997 \$14339 stype fragment
Iq gamma-1 chain precursor (1505) - mouse (fragment)
efformal\_name Kus musculus \*common\_name house mouse
55-pb-1394 sequence\_revision 10-Nov-1395 stext\_change
103-sp-1397 -114329 No. J.A.; Bona, C.A.; Rolmdahl, R.
Bur. J. Immunol. (1993) 23:2503-2510
Variable region gene selection of immunoglobulin G-expressing
B cells with specificity for a defined epitope on type II ddamme, A.M.; Bulens, F.; Bernar, H.; Melles, L.; Lijnen, 4.H.; Collen, D 5. J. Biochem. (1990) 192:767-775 0; Mismatches 0 Indels 0; Gaps Gaps homology 0 0

Obery Match 13:15; Score 20: DB 2: Length 102; Best Local Similarity 100:0%; Prdd. No. 4:96e-28; Matches 20; Conservative 0; Mismatches 0; Indels 0;

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Mon Apr 19 13:23:59 1999

RESULT 12
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ACCESSIONS REFERENCE #authors PNO444 "type fragment Ig heavy chân V region precursor - human (fragment) #formal\_name Homo sapiens #common\_name man 30-Sep-1993 #equence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

\*journal Gene (1992) 122:321-328
A general method for chimerisation of monoclonal antibodies
by inverse polymerase chain reaction which conserves
authentic N-terminal sequences. Kaluza, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle, U.H.

\*\*modecule\_type mRNA
\*\*residues 1-132 \*\*label BUC
\*\*residues 1-132 \*\*label BUC
\*\*\*REFERENCE 970410 GB:ML6163; NID:g195405; PID:g195406

Lebecque, S.G.; Geathart, P.J.
2 Exp. Med. (1990) 172:1717:1727

Boundard sof sometic nutation in rearranged immunoglobulin geners, boundary as near the promoter, and 3' boundary is about 1 kb from Y(D)J gene.

\$70410

Page 30

34-117 SUMMARY

\*\*accession profession 
20-117 SUMMARY edomain signal sequence estatus predicted #label SIGN #product ig heavy chain V region #status predicted #label MAT. #domain variable region #label VRG #length 150 #checksum \$720

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RESULT 13 ENTRY TITLE ORGANISM DATE B04471 stype complete
Ig heavy chain precureor V region (MAR3) - mouse
formal\_name Mus\_musculus ecommon\_name house mouse
65-Jun-1988 sequence\_revision O5-Jun-1988 stext\_change
207-Mug-1998
207-Mug-1990
824471; 570410

P.; Hubner-Parajez, C.; Mattes, R.; Lenz, H.; Haug. Beaucamp, K.

ACCESSIONS REFERENCE \*authors

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ORGANISM DATE ACCESSIONS REFERENCE @authors #journal etitle RESULT 15 ENTRY TITLE S06824 stype complete
Ig heavy chain v region (clone 1204) - mouse
dformal\_name Mus musculus \*common\_name house mouse
30-Sep-1991 sequence\_revision 11-Nov-1994 stext\_change
08-Sep-1997

authors Miller III, A.; Glasel, J.A.

spoundl J. Mol. Biol. (1989) 209:753-778

ettle Comparative sequence and immunochemical analyses of murine
monoclonal anti-morphine antibodies.

secoss:references MID:90064531

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semblecute\_type mRNA
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CLASSIFICATION KEYWORDS FEATURE 15-98 #superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin

22-96 SUMMARY Query Match Best Local S Matches 1 h 11.8%; Similarity 100.0%; 18: Conservative #domain immunoglobulin homology #label IMA\
#disulfide\_bonds #status predicted
#length 124 #molecular-weight 13871 #checksum 1710 Score 18; DB 2; Length 124; Pred. No. 3.01e+23; 0; Mismatches 0; Indels 0;

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Submour, R.
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839594 ftype fragment
Ig gamma chân (#985) - mouse (fragment)
fformal\_name Mus musculus fcommon\_name house mouse
06-Jan-1995 fsequence\_revision 06-Jan-1995 stext\_Change
10-Sep-1997

Ouery Match 12.4; Score 19; DB 2; Length 152; Best Local Similarity 100 09; Pred No. 1.25e-25; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps

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ig heavy chain V region nouse

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Ig gamma chain - mouse
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19-May-1994 @sequence\_revision 10-Nov-1995 @text\_change
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bbert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bitter-Suermann, D.; Hilschmann, N.

Hilechmann, N.

Biol. Chem. Hoppe-Seyler (1993) 374.993-1000
Primary structure of the murine monoclonal 1952a antibody mbb75s spaints alpha(7-0) polystalic acid. 2. Amino acid sequence of the heavy (H-)chain fd' region.

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*Hilschmann, N.;

*submission submitted to the EMSI Data Library, January 1993

*description Primary structure of the murine monoclonal 1952a antibody mab735 against (2-8) polystait acid. 2. Maino acid eaccession $40285
*Authors Nilinger, L. | Spidata, T. / Ozaki, S. ; Shirai, T. / Jaton, # Spound | Bur J. Immunol, (1990) 20:771-777

**Lite Variable region isequences of pathogenic anti-mouse red blood cross-references MPID:90269318

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disulfide bond; glycoprotein; immunoglobulin; pyroglutanic
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Ig gamma-la chall (mbh75) - mouse
formal_name Mus musculus *common_name house mouse
7-Apr-1994 *sequence_revision 07-Apr-1994 *text_change
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#length 246 #molecular-weight 26216 #checksum 7059
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J. Exp. Mcd. (1993) 117.797-809

Hypermutation is observed only manufactured in the endogenous immunoglobulin H DNN: Implications for the location of cis-acting elements required for somatic mutation.

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**molecule_type mRNN
**residues 1-100 **slabel 71L
**residues 1-100 **slabel 71L
**residues 1-100 **slabel 71L
**cassperimental_source B cell_strain [NZB x NEW]Fl
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J. Exp. Med. (1992) 176.761.779
Both 15M and 19G anti-DNA antibodise are the produces of clonally selective B cell stimulation in (NEB x NEW)F1
mice.
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PH0999 stype fragment
Ig heavy chain V region (clone 165.3) - mouse (fragment)
sformal_name Nus musculus scommon_name house mouse
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Ouery Match 10.5%; Score 16; DB 2: Length 116; Best Local Similarity 100.0%; Pred. No. 1.42e-19; Matches 16; Conservative 0; Mismatches 0; Indels Indels 0; Gaps

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PHISI2 \*type fragment
Ig heavy chain v region (clone X7-5D3-18) - mouse (fragment)
#formal\_name Hus musculus \*common\_name house mouse
03-Feb-1994 \*text\_change
16-Ng-1996
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GLUBELL A. M.: Maneer, T.

ssuperfamily immunoglobulin V region: immunoglobulin homology heterotetramer; immunoglobulin

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						Page 37
RESULT 26  PLO242 stype fragment TITLE 19 heavy chain v region (anti-DNA, SS4VH) - mouse (fragment) ORANISH stormal.name Aus musculia scommon_name house mouse house DATE 16-Sep-1992 sequence_revision 16-Sep-1992 stext_change 16-Aug-1996 ACCESSIONS pLO242 REFERENCE PLO231 Resulthore Shlomchik, M.: Mascelli, M.: Shan, H.; Radic, M.Z.: Pisetsky,	Query Match 9 8%; Score 15; DB 2; Length 67; Best Local Similarity 100 0%; Pred. No. 2.73e-16; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Db 53 SLINSEDSAVIPCAR 67	*Accession K18833 WARRY A CASSIFICATION **STREAM *	J. I	RESULT 25  RESULT 25  RESULT 25  RESULT 19 kappa chair V tegion (RP22.202.16) - mouse (fragment)  ORGANISH SCHMAL, Dame Hum musculus Scommon, name house mouse  DATE 30-Sep-1899 Sequence_revision 30-Sep-1899 Stext_change  O-May-1897  ACCESSIONS H3833  REFERENCE 18983  REFERENCE NS. Bitt. M.: Roth C. These 7. Emission NS. Sep-1899	Ouery Match initarity 100.0%; Score 15: DB 2: Length 43: Best Local Similarity 100.0%; Pred. No. 2.73e-16: Matches 15: Conservative 0: Mismatches 0: Indels 0: Gaps 0: Db 4 SSITSDSAVFCAR 18 Cy 103 SSITSDSAVFCAR 117	Mon Apr 19 13:23:59 1999 US-08-836-455-4.zpr

# Journal J. Exp. Marshak-Rothstein, A.; Weigert, M. # etitle Anti-DRA antiodes from autoimnume mice arise by clonal ecosa-reference Expansion and sometic mutation.

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AUTHORS

AUTHORS

Sherman, M.A.; Deans, R.J.; Bolger, M.B.

JOURNAI

ALOPETIGOL binding to monoclonal antibodies. Hypervariable

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Query Match 9.8%; Score 15; DB 2; Length 96; Best Local Similarity 100.0%; Pred. No. 2.73e-16; Matches 15; Conservative 0; Mismatches 0; Indels 0 Gaps

RESULT 27
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G35513 etype fragment
Ig heavy chain v region (BNN14) mouse (fragment)
ig heavy chain v region (BNN14) mouse (fragment)
ig heavy chain v region (BNN14) mouse mouse
21-May-1990 sequence\_revision 31-Dec-1990 \*text\_change
116-Nuv-1996
12551

ACCESSIONS REFERENCE \*authors

RESULT 29 ENTRY TITLE ORGANISM DATE PHIO02 \*type fragment
Ig heavy chain Y region (clone 165.45) - mouse (fragment)
if cormal\_name Mus musculus \*common\_name house mouse
30-Sep-1993 \*sequence\_revision 30-Sep-1993 \*text\_change
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KOILER, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.;

ROOMAN, D.J.; Duchosal, M.A.; Dixon, F.J.; Theofilopoulos,

\*Sournal J. Clin, Invest. (1988) 82:852-860

\*Filte Immunojlobulin kappa light chain variable region gene complex

organization and immunoglobulin genes encoding anti-DNA

\*\*Erros. reference RMID: 88311394

\*\*\*accession 033213

\*\*\*molecule\_type DNA

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\*\*\*RESIDUES \*\*\*

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\*\*\*PROPRIES\*\*

\*\*\*CLASSIFICATION \*\*\*superfeamily immunoglobulin V region; immunoglobulin homology KETWORDS

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J. Exp. Hed. (1992) 16:781-779
Goth IgM and igG anti-DNA antiBodies are the products of clonally selective B cell stimulation in (MZB x MZB)F1
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Query Match 9.8%; Best Local Similarity 100.0%; Matches 15; Conservative Score 15; DB 2; Length 106; Pred. No. 2.73e-16; 0; Mismatches 0; Indels 0;

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RESULT 30 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE Sauthors PLO240 \*type fragment Ig heavy chain V region (anti-DNA, 557VB) - mouse (fragment) \*formal\_name Nus musculus \*common\_name house mouse 16.5ep-1992 \*sequence\_revision 16.5ep-1992 \*text\_change 16.4mg-1996

\*journal hlomohik, M.; Mascelli, M.; Shan, H.; Radic, M.E.; Pisstaby, D.; Marshak-Robhstein, A.; Peigest, M. C. Exp. Med. (1990) 171:265-297 inti-DNA antibodies from autoimmune mice arise by clonal expansion and sonatic mutation.

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RESULT 32
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16 neary chain was mouse. Tevision 13 Jan-1995 steat\_change
16 neary chain was mouse 
ACCESSIONS REFERENCE \*authors \*journal \*title

Stark, S.E.; Gaton, A.J.

3. Exp. Med. (1991) 174:613-624

Antibodies that are specific for a single amino acid
interchange in a protein epitope use structurally distinct
variable regions.

\*Accession 82616
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Query Match 9.8%; Best Local Similarity 100.0%; Matches 15; Conservative Score 15: DB 2; Length 108; Pred. No. 2.73e-16; 0; Mismatches 0; Indels 0; Caps

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72.

RESULT 33
ENTRY
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DATE 19097 stype fragment

2 heavy hat net retion (clone 17s-c); mouse (fragment
2 heavy hat net retion (clone 17s-c); mouse source
30 depty 30 sequence retiiion 30 dep 1993 steat\_change
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16 heavy sequence retiiion 30 dep 1993 steat\_change

mouse (fragment)

ACCESSIONS REFERENCE \*Authors \*journal \*title 

status nucleic acid sequence not shown molecule\_type mRNA | residues 1-109 selabel TIL

Page 43

Mon Apr 19 13:23:59 1999

Query Match 9.8%; Score 15; DB 2; Length 109; Best Local Similarity 100 0%; Pred. Wo. 2.73e-68; Matches 0; Indels Matches 15; Conservative 0; Mismatches 0; Indels 0

RESULT 34
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TITLE
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PHINOO etype fragment
Ig heavy chair v region (clone 202.105) - mouse (fragment)
if theavy chair v region (clone 202.105) - mouse mouse
if cormal\_name Mus museulus ecomon\_name house mouse
30-Sep1993 esequence\_revision 30-Sep-1993 etext\_change
16-Aug-1996

ACCESSIONS REFERENCE \*authors \*journal \*title

Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. (1992) 176:761-779
Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell stimulation in (NEB x NEW)F1

\*eccession PH1000
\*estatus PH1000
\*estatus nubleic acid sequence not shown
\*molecule\_type mRN,
\*residues 1-110 \*slabel TIL
\*residues 1-110 \*slabel TIL
\*residues 1-110 \*slabel TIL
\*residues 1-110 \*slabel TIL
\*\*residues 1

Query Match Best Local S Matches 1 h 9.8%; Similarity 100.0%; 15; Conservative #domain immunoglobulin homology #label IMM #length 110 #checksum 377 Score 15; DB 2; Length 110; Pred. No. 2.73e-16; 0; Mismatches 0; Indels 0;

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526317

stype fragment

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Page 42

87-97 98-107 SUMMARY #region complementarity-determining 3\
#region framework 4
#length 107 #checksum 7469

Db 72 SSLTSEDSAVFCAR 86 Query Match 9.8%; Score 15; DB 2; Length 107; Best Local Similarity 100.0%; Pred. No. 2.73e-16; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0

PLO241 \*type fragment
Ig heavy chain v region (arti-DNA, 841VH) - mouse (fragment)
formal\_name Mus musculus \*common\_name house mouse
16-Sep-1992 \*text\_change
16-Nep-1993 \*ext\_change

RESULT 31 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE \*authors Shiomichik, M.: Mascelli, M.: Shan, H.: Radic, M.Z.: Pisetaky,
D.: Marshak-Rochisetin, A.: Weigert, M.
ZEXP, Mach (1990) 171:265-297
Anti-DRA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.
The apparaison and somatic mutation.
The apparaison and somatic mutation.
The apparaison and somatic mutation.

scross-references MU saccession PL0241 -7-7-1-107 selabel SHL segion: immunoglobulin homology heterotetraner; immunoglobulin v region: immunoglobulin homology

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Page 44

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ACCESSIONS REFERENCE \*authors \*journal \*title

TITLE ORGANISM DATE

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Gaps

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Fauthors Rininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton,

J.C.; Izui,
J.C.; Izui,
J.C.; Izuinol. (1990) 20:771-777

*title Variable region sequences of pathogenic anti-mouse red blood

*cross-references MULD-90269328

*cross-references MULD-90269328

*accession S99917

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**molecule_type_mRNA,
**residue_type_mRNA,
**residue_type_mRNA,
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**CLASSIFFCATION **superfamily immunoglobulin V region; immunoglobulin homology
ECPMONES heterotetramer; immunoglobulin
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Best Local Similarity 100.0% Pred No. 278-16;
Matches 15; Conservative 0; Missatches 0; Indels 0;
#accession 955535
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##molecule_type mRNA
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855535
                                                                                                                                                                          Bootigor, V.; Bootigor, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. (1995) 347:92-946
Comprehensive epitope analysis of monocional
anti-proencephalm antibodies using phage display libraries
and synthetic pepides: revelation of antibody fine
specificities caused by somatic mutations in the variable
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Ig heavy chain v region pe23 - mouse (fragment)
formal_name Nus musculus scombol_name house mouse
27-opt-1995 secquence_revision 03-Nov-1995 stext_change
_08-Sep-1997
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*length 112 *checksum 334
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Ig heavy chain VD-J region (106-102) - mouse (fragment)
*formal_name Mus musculius *common_name house mouse
12-Feb-1993 *sequence_revision 12-Feb-1993 *fext_change
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19 heavy chain V region (geminal centre B17 DNA Rr.4 and
others). mouse (fragment),
eformal_name Nua musculus (common_name house mouse
25-reb-1994 sequence_revision 01-bec-1995 *text_change
03-bep-1997 sequence_revision 01-bec-1995 *text_change
03-bep-1997 sequence_revision 01-bec-1995 *text_change
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submitted to the EMBL Data Library, July 1992
In situ studies on the primary immune response to
(4-hydroxy 3-nitrophenyl)acetyl. II. A common clonal origin
for periarteriolar lymphoid sheath associated foci and
germinal centres.
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v. Exp. Med. (1991) 174:613-624
Antibodies that are specific for a single maino acid
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#Cormal_name Hus musculus #common_name house mouse
19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change
17-Apr-1998
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### SUperfidential_source germinal centre B17 DNA Nr.6
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Similarity 100.0%; Pred. No. 2.73e-16;
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submitted to the EMBU Data Library, July 1992
In situ studies on the primary immune response to
(a-hydray-3-mitropheny))scetyl. II. A common clonal origin
for periarteriolar lymphoid sheath associated foci and
germinal centres.
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Ig heavy chain v region anti-triplex DNA - mouse (fragment)

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ACCESSIONS REFERENCE \*Authors PLO218 "type fragment Ig heavy chain V zegion (anti-DNA, 6WVH and 6QVH) - mouse If tagment; discommon\_name house mouse formal\_name kns musculus frommon\_name house mouse 16-Sep-1992 destroyange 16-App-1996 aren's page 1996

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Ig heavy chain V region (arti-DNA, IAI1VH) - mouse (fragment)
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omchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, .; Marahak-Rochatein, A.; Weigest, M. Exp. Med. (1999) 171:265-297

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ACCESSIONS REFERENCE Pauthors Shoochit, M.; Mascelli, M.; Shan, H.; Radic, M.2.; Pisetaky,
D.; Masshar-Spottacein, A.; Weigert, M.
J. Exp. Red. (1990) 171:265-297
Anti-DNA antibodies from autoLimune mice arise by clonal necession and somatic mutation.
necession and somatic mutation.
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Ig heavy chain v region (arti-DNA, D20VH) · mouse (fragment)
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*journal H. P.; Quesniand, (1907) 27:1029-1038

*Ithe Analysis of the structural diversity of monocional antibodies

*cross-references MDID: 91042649

*acession: PROOF 8M

**CLASSIFICATION **

**Extraction **

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J. Biol. Chem. (1988) 653-4059-405.
Haloperido; binding to monoclonal antibodies. Hypervariable
region main code advence determination.
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sformal_name Haus musculus *common_name house mouse
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Ig heavy chain V region (anti-cyclosporin A) - mouse
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#formal_name Mus musculus *foommon_name house mouse
15-Jan-1993 *sequence_revision 15-Jan-1993 *text_change
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#inter, E.; Radbruch, A.; Krawinkel, U.
BEBO J. (1985) 4:2861-2867

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Best Local Similarity 100.0%; Pred. No. 4.69-17;
Matches 14; Conservative 0; Kismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE D AND J SECREMYS.

-I THIS PROTEIN BINNS DEXTRAN.

PER: A36242 MHSSJ. SEVEN.

HSSP: POLTOS; ZEVEN.

HSSP: POLTOS; ZEVEN.

LYMINOCLOBULIN V ROJION.

DINGUERD 12 95 BY SIMILARITY.

SCHURKE 117 AA: 13024 MF: E7548A05 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TWYL2 JOUSE STANDARD; PRT: 117 AA.

11.7UZ. 1986 (REL. 01, CREATED)
11.7UZ. 1986 (REL. 01, CAST SEQUENCE UPDATE)
11.7UZ. 1988 (REL. 01, LAST SEQUENCE UPDATE)
11.7UZ. 1988 (REL. 02) LAST ANNOTATION UPDATE)
12.8UY. CHART RELON (MOPE 104E).
13.8UY. CHART RELON (MOPE 104E).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-836-455-4.rsp
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CCCRP RESULT
                                                            ENGURACE, 80078170.

SCHILLING J., CLEVINGER B., DAVIE J.H., HOOD L.;

SCHILLING J., CLEVINGER B., DAVIE J.H., HOOD L.;

MATURE J83:35-40(1980).

1- THE SEQUENCES OF 10 HYBRIDONA PROTEINS THAT ALSO BIND DEXTRAN-
DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN
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ALIGNMENTS

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Page
         Mon
                                                                                                                                                                                                                                                                            A MEDIUME 10075344.

MARTINE 10075344.

MARTINE 18.075744 15., SCHILLING J.W., ROCERS J., SIBLEY C.H.,

MARTINE 18. PORRAM J.S., SCHILLING J.W., ROCERS J., SIBLEY C.H.,

MARTINE 18. PORRAM 15.5424 (1982).

C. 1. THE SECUENCE OF THE LIGHT CHAIN OF THIS ICH MYELONA PROTEIN HAS C.I. THE SECUENCE OF THE LIGHT CHAIN OF THIS ICH MYELONA PROTEIN HAS C.I. THE SECUENCE HASAE.

PIR. HASD POLITIC: IFOUR PROTEIN PROTEIN PROTEIN TO LIGHT 12. PROTEIN PROTEIN TO LIGHT 11. 17.

PROLITER 117 AN: 12983 MP: 1F6CC304 CRC32;

SCOURNCE 117 AA: 12983 MP: 1F6CC304 CRC32;
                                                                                                                                                                                  8
      Apr 19 13:24:00 1999
                                                                                                                                                                                                                 Query Match 9.2%;
Best Local Similarity 100.0%;
Matches 14; Conservative
                                                                                                                                                     15 GASVKMSCKASGYT 28
                                                                                                                                                                                                                 Score 14; DB 1; I
Pred. No. 4.69e-17;
0; Mismatches (
US-08-836-455-4.rsp
                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                   Length 117;
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                 0
                                                                                                                                                                                                                 Gaps
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RESULT 5

DRIVER STANDARD; PRT: 144 AA.

AC 901935, 101, CREATED)

DT 21-JUL-1986 (REL. 01, CREATED)

DT 21-JUL-1986 (REL. 01, CAST SEQUENCE UPBATE;

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPBATE;

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPBATE;

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPBATE;

DE 101-SEQUENCE LA 1, LAST SEQUENCE UPBATE;

DC HEAVE CHAIN PRECURSOR V REZION (NODE 141).

OC EUTRALIELLA: RODERNIA

RN 11]

RN 12]

RN
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Best Local Similarity 100.0%;
Matches 14; Conservative
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CAPRA J.D.,
CAPRA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14; DB 1; Len
Pred. No. 4.69e-17;
0; Mismatches 0;
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HVOLMOUSE STANDARD; PRT; 120 AA.

PO.747;

12.-UU-1966 (REL. 01, CREATED)

21.-UU-1966 (REL. 01, LAST SROUENCE UPDATE)

21.-UU-1966 (REL. 01, LAST ANNOTATION UPDATE)

10. LAST ANNOTATION UPDATE

10. LAST ANNOTATION UPDATE;

10. LAST ANNOTATION UPDATE;

11. LAST ANNOTATION UPDATE;

12. LAST ANNOTATION UPDATE;

13. LAST ANNOTATION UPDATE;

14. LAST ANNOTATION UPDATE;

15. LAST ANNOTATION UPDATE;

16. LAST ANNOTATION UPDATE;

17. LAST ANNOTATION UPDATE;

17. LAST ANNOTATION UPDATE;

18. LAST ANNOTATION UPDATE;

18. LAST ANNOTATION UPDATE;

18. LAST ANNOTATION UPDATE;

18. LAST ANNOTATION UPDATE;

19. LAST ANNOTATION UPDA

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34 GASVKMSCKASGYT 47

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WELLINE: 93111846.

AKEDLINE: 93111846.

AKEDLINE: 93111846.

AKEDLINE: 93111846.

AKEDLINE: 93111846.

AKERATI HI, GEFFER H.L., BRODEUR P., RIBLET R.,

AKHARSAK-ROCHSTEIN A.,

BE EER. J. INTRODELL ISTORY 1032(1992).

CC THAT THRESIDIET OF THE SIZES OF SEVERAL OTHER DIPPERENTIATED GENERAL THRESIDIET OF THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J SEGMENT, JH2.

DR PER, 102028: HYMSGT. THE SAME J SEGMENT, JH2.

BR HSSP, PO1799; 6FAB.

KM INCHMOGLOBULIN V REZION; ANTIARSONATE ANTIBODY; HYBRIDONA.

SO SEQUENCE 120 AA; 11307 MH; BBASCAL CRC22;

RESULT AC POT 21 DT 21 D

SEQUENCE FROM N.A. STRAIN=A/J; MEDLINE: 82152818.

Query Match 9.2%; Score 14; DB 1; Ler Best Local Similarity 100.0%; Pred. No. 4.69e-17; Matches 14; Conservative 0; Mismatches 0;

Length 144;

0

Gaps

TWYO2 MOSSE STANDARD: PRT: 140 AA.

107136 (REL. 01, CREATED)
21.-UL-1986 (REL. 01, CREATED)
21.-UL-1986 (REL. 01, CREATED)
21.-UL-1986 (REL. 01, ASS RECORNCE UPDATE)
21.-UL-1986 (REL. 01, ASS RECORNCE)
21.-UL-1986 (REL 01, ASS RECORNCE)
21.-UL-1986 (REL. 01, ASS RECORNCE)
21.-UL-1

ő 문

84 SLTSEDSAVYFCAR 97 |||||||||||| 104 SLTSEDSAVYFCAR 117

Query Match Best Local S Matches 1

h 9.2%; Similarity 100.0%; 14; Conservative

Score 14: DB 1: Length 120: Pred. No. 4.69e-17; 0: Mismatches 0: Indels 0;

Gaps

0

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Page 26

HAMMALIA:

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131 LDYWGQGTSVIVSS 144 |||||||||||||||| 124 LDYWGQGTSVIVSS 137

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5 B
                                        Query Match 8.5%;
Best Local Similarity 100.0%;
Matches 13; Conservative
                                                                                                                                                                                                                       ADETUGBO K., MILSTEIN C., (
NATURE 265:299-304(1977)
EMBL: JO0522: G195055; -
PIR: AD2066; GIMS21.
HSSP: P01607: 1FGV
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 81234548.
BOTHWELL A.L.M., PASKIND M.,
BALTIMORE D.;
                                                                                                                                                                                                                                                                                                                                                                   TIVE AUGUSE STANDARD: PRT; 136 AA.

12.7UI-1986 (REL. 01, CREATED)

21.7UI-1986 (REL. 01, LAST SEQUENCE UPDATE)

21.7UI-1986 (REL. 01, LAST ANNOTATION UPDATE)

21.7UI-1986 (REL. 01, LAST ANNOTATION UPDATE)

32.7UI-1986 (REL. 01, LAST ANNOTATION UPDATE)

33.7UI-1987 (REL. 01, LAST ANNOTATION UPDATE)

34.7UI-1987 (REL. 01, LAST ANNOTATA; TETRAPODA; HU

EURANGE, ROCCESTIA.

1017HERIA; ROCCESTIA.
LL 24:625-637(1981).
                                                                                                                                                                                                            LOBULIN V REGION; SIGNAL
                                                                                 115
120
136
136
136
136
136
130
130
130
130
130
130
                                                                                 15071 MW;
                                                                                                                                                                                                                                                                SECHER D.S.;
                                                                             HYAD -> DYAH (IN REF. 2).
DN -> ND (IN REF. 2).
W -> H (IN REF. 2).
Y -> W (IN REF. 2).
Y -> W (IN REF. 2).
                                     Score 13: DB 1: Length 136:
Pred. No. 1.75e+14;
0: Mismatches 0; Indels
                                                                                                                                                        IG HEAVY CHAIN V REGION (MOPC D SEGMENT.
JH4 SEGMENT.
                                                                                                                                                                                                                                                                                                                          IMANISHI-KARI T., RAJEWSKY K.
                                                                                                                                                                                                                                                                                                                                                                                HAMMALIA:
                                        0
                                        Gaps
                                        0
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ATIA.

ADM N.A.

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21.-UL-1986 (REL. 01, CREATED)
21.-UL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01.-NOV-1980 (REL. 16, LAST ARROTATION UPDATE)
10. HAVY CHAIR PRECURSOR V RECION (107).
NUS MUSCULUS (MOUSE).
ULARYOTA, METADOA: CHONDATA: VENTEBRATA: TETRA-PODA;
CUTHERIA: RODENTIA.
                117
12867 MW; 4BDD1982 CRC32;
                                                                                                                                        IG HEAVY CHAIN V REGION (102).
FRAMEWORK I TO ETERMINING 1.
FRAMEWORK 2.
FRAMEWORK 2.
FRAMEWORK 2.
FRAMEWORK 2.
FRAMEWORK 2.
FRAMEWORK 2.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTIBODIES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENES
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RESULT POR SOLUTION OF THE SOL

ID HYOL, MOUSE STANDARD; PRT: 117 AA.

KC P01748:

YT 21-UU-1986 (REL. 01, CREATED)

YT 21-UU-1986 (REL. 01, LAST SEQUENCE UPDATE)

YT 01-10V-1996 (REL. 12, LAST SEQUENCE UPDATE)

YT 01-10V-1996 (REL. 01, LAST SEQUENCE UPDATE)

YT 01-10V-1996 (REL. 01, LAST SEQUENCE)

YT 01-10V-1996

MAMMALIA;

SECURECE PROM N. A.
HEDLINE 8 1145315 . REPRON R.
CTOL D. SAKUT N. EFFRON R.
NATURE 202 426 440(128) .
PIN 100488 . C550(28) .
PIN 100488 . LTG
HSSP: P01789 . LTG

RECHAVI

ON UPDATE)

TETRAPODA;

MAMMALIA

117 AA

NOGLOBULIN V REGION; SIGNAL 1 19

5 g

Query Match 7.2%;"|
Best Local Similarity 100.0%;
Matches 11; Conservative

Score 11; DB 1; Len Pred. No. 1.54e-09; 0; Mismatches 0;

Length 117; Indels

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Gaps 0 Mon

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RESULT 8
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                            106 YMGQGTSVTVSS 117
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126 YMGQGTSVTVSS 137
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Query Match 7.8%;
Best Local Similarity 100.0%;
Matches 12; Conservative
STANDARD;
                           Score 12; DB 1; Ler
Pred. No. 5.66e-12;
0; Mismatches 0;
PRT;
117
                                                                 FROM A MYELOMA PROTEIN.
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                                  Length 117;
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Best Local Similarity 100.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SULT 100SE STANDARD: PRT: 117 AA POLTSS: 117-14-190SE (REL. 01, CREATED) 21.-UU.-1986 (REL. 01, LAST SEQUENCE UPDATE) 01.-CT-1986 (REL. 01, LAST SEQUENCE UPDATE) 10-CT-1986 (REL. 01, LAST SEQUENCE UPDATE) 11-CT-1986 (REL 01, LAST SEQUENCE UPDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BALTIMORE D. ...
CELL 24:625-637(1981).
CELL 24:625-637(1981).
CELL 24:625-637(1981).
FIS GERLINE GENE BELONGS TO A SET THAT COULD ENCODE V REGIONS OF NPB A PIR: A02005; NFMS23.
HSSP: P01810; 1JHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-C57BL/6;
MEDLINE: 81234548.
BOTHMELL A.L.M., PASKIND M., RETH M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 PGQGLEWIGNI 70
|||||||||||
60 PGQGLEWIGNI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 IG HEAVY CHAIN V RE.
44 PRAMEMORY 1.
54 OPPLEMENTATIVE DET!
56 PRAMEMORY 2.
66 PRAMEMORY 2.
67 PRAMEMORY 1.
115 PRAMEMORY 1.
117 BY SHILLARITY.
117 MY 66834DIA CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IG HEAVY CHAIN V REGION (23).
PRANTHOUR: ...
COMPLEMENTARITY-DETERMINING 1.
PRANTHOUR: ...
COMPLEMENTARITY-DETERMINING 2.
PRANTHOUR: ...
PRANTHOUR: ...
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMANISHI-KARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTIBODIES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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  CHAIN
NON_TER
SEQUENCE
20
117
117 AA;
                IG HEAVY CHAIN V REGION (10A)
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Page 30

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Query Match 7.2%;
Best Local Similarity 100.0%;
Matches 11; Conservative
103 SSLTSEDSAVY 113
{||||||||||
103 SSLTSEDSAVY 113
                                                                    117 IG
117
; 12972 MW;
                                  941C002E CRC32;
                                   Gaps
                                   0
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RY4_MOUSE STANDARD: PRT: 117 AA.
P06328:
01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-WOY-1980 (REL. 16, LAST SEQUENCE UPDATE)
10 HAVY CHAIN PRECURSOR V RECION (VHSS 84).
MUS MOSCULUS (MOUSE).
EURAROTA: NORTHER ADMINISTRATION PROTECTION (VHSS 84).
10 HARMELL NORTH (MOUSE).
10 HARMELL NORTH (MOUSE).
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IG REMY CHAIN V REGION (VHSS8 BI PRAMEMORA, INC. COMPLEMENTATITY-DETERMINING 1. PRAMEMORA, 2. PRAMEMORA, 2. PRAMEMORA, 3. BY SIMILARITY.

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ő
                B
                                    Query Match 7.2%;
Best Local Similarity 100.0%;
Matches 11; Conservative
103 SSLTSEDSAVY 113
                                  Score 11: DB 1: Length 117;
Pred. No. 1.54e-09;
0; Mismatches 0; Indels
                                    0
                                    Gaps
                                    0
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P SEQUENCE PROM N.A.

REDUENCE PROM N.A.

RESEP POUBLE, 141EL.

PRINCE ACCOSS, HEMSEN.

REDUENCE PROM N.A.

RESEP POUBLE, 141EL.

RESEPONE.

                                                                                                                     12834 MW; 85692FE5 CRC32;
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RESULT
ID PO
PO
DT 211
DT 011
DT 011
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.2%;
Best Local Similarity 100.0%;
Matches 11; Conservative
HYO 130 STANDARD; PRT; 117 AA.

BYO_DOUSE STANDARD; PRT; 117 AA.

BYO_TS4; PS1270;
21-7UL-196 (REL. 01. CREATED)

O1-7UL-1969 (REL. 11. LAST SECURNCE UPDATE)

O1-7UL-1969 (REL. 34. LAST ANOTATION UPDATE)

IG HEAVY CHAIN PRECURSOR V REGION (145).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOT 12

RVO5_MOGNE STANDARD; PRT: 117 AA.
P07.749;
21.-UL-1986 (REL. 01, CREATED)
21.-UL-1986 (REL. 01, LAST ESQUENCE UPDATE)
01.-CT-1986 (REL. 04, LAST ESQUENCE UPDATE)
10 HEAVY CHAIN PRECUBSOR V REGION (3).
MUS MUSCULUS (MOUSE)
MUS MUSCULUS (MOUSE)
EUTARICOTA. METAEDA. CRORDATA: VERTEBRATA: TETRAPODA:
DUTHRETA: ROBERTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE: 81334548.
BOTHRELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
BALTIMORE D.:
                                                                                                                                                                                                                                                                                  60 PGQGLEWIGNI 70
|||||||||||
60 PGQGLEWIGNI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :625-637(1981).
15 GERDLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
17 COULD ENCODE Y RECIONS OF NPB ANTIBODIES.
100536; G554035; •.
20011, NPMS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1
20
20
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55
69
69
117
NA;
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N Y REGION: SIGNAL.

20 117 IG H
20 44 PRAM.

50 54 COMP
55 66 PRAM.
66 117 PRAM.
61 115 PRAM.
61 115 PRAM.
62 117 PRAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13016 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG HEAVY CHAIN V REGION (3).
PRACESORS. ..
COMPLEXENSATIV-DETERMINING 1.
PRACESORS ..
COMPLEXENSATIV-DETERMINING 2.
PRACESORS ..
PRACESORS ..
PRACESORS ..
PRACESORS ..
PRACESORS ...
PR
                                                                                                                                                                                                                                                                                                                                                                                           Score 11; DB 1; Length 117;
Pred. No. 1.54e-09;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF12FC8B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAMMALIA:
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Query Match 7.2%;
Best Local Similarity 100.0%;
Matches 11; Conservative
103 SSLTSEDSAVY 113
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EUKARYOTA: METAZOA; CHORDATA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=C57BL/6;
STRAIN=C57BL/6;
BOTHWELL A.L.M., PASKIND M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             625-637(1981).

GENCLING GENE BELONGS TO A SET COULD ENCODE V REGIONS OF NPB A 10531; G554033; G554033; G554033; G554031; G5540315; G554031; G554031; G554031; G554031; G554031; G554031; G55403
                                                                                                                                                                                                                                                                                                                                                                                                                                                117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE. SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                        12921 MW; D9E6B000 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG HEAVY CHAIN V REGION (145).
PRAMEMORK 1.
COMPLEMENTARITY-DETERMINING 1.
PRAMEMORK 2.
COMPLEMENTARITY-DETERMINING 2.
PRAMEMORK 3.
                                                                                                                                                                                                               Score 11; DB 1: Length 117;
Pred. No. 1.54e-09;
0; Kismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RETH M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMANISHI-KARI T., RAJEWSKY K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTIBODIES.
                                                                                                                                                                                                               0
                                                                                                                                                                                                               Gaps
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8 Ś

SEQUENCE FROM N.A.
MEDILNE: 81053741.
ARDIT R., COMEN J., GIVOL D.;
NUCLEIC ACIDS RES. 8:3591-3601(1980)
[2]

HVOLIGOUSE STANDARD: PRT: 121 A.

PO1745:

12.-UU-1966 (BEL. 01, CREATED)

21.-UU-1966 (BEL. 01, CREATED)

13.-UU-1966 (BEL. 01, CREATED)

13.-UU-1966 (BEL. 01, CREATED)

13.-UU-1966 (BEL. 01, CREATED)

13.-UU-1966 (BEL. 01, CREATED)

16.-UU-1966 (BEL. 01, CREATED)

16.-UU-1966 (BEL. 01, CREATED)

17.-UU-1966 (BEL. 01, CREATED)

18.-UU-1966 (BEL. 01, CREATED)

19.-UU-1966 (BEL. 0

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                                                                                                           STERRICCERR
                                                    Query Match
Best Local S
Matches 1
                                                                                                 ** REVISIONS.

** ARAUT R. COMEN J. GIVOL D.

** NUCLEIC ACIDS RES. 8:4839-4840(1980).

** ITHIS SEQUENCE MAS THANSATED FROM AN

** ITHIS SEQUENCE MAS THANSATED FROM A

** PIR: ACCOLD AFFE.

** RESP: POISIO. 14FE.

** IMMUNOCLOSULIN Y RESIN.

** IMMUNOCLOSULIN Y RESIN.

** IMMUNOCLOSULIN Y RESIN.

** SEQUENCE 121 AA: 13115 MM; 2ASFC8CC
70 LTADTSSSTAY 80
||||||||||||
89 LTADTSSSTAY 99
                                            7.2%; £
1 Similarity 100.0%; F
11; Conservative
                                                  Score 11: DB 1: Length 121: Pred. No. 1.54e-09; O: Mismatches 0: Indels
                                                                                                         2A8FC8CC CRC32;
                                                                                                                                                                                       AN MRNA
                                                                                                                                                                                         ISOLATED
                                                    0
                                                  Gaps
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RESULT 15

RESULT 15

RESULT 15

RESULT 15

ROTES STANDARD: PRT: 137 AA.

AC PRITSSOURCE STANDARD: PRT: 137 AA.

AC PRITSSOURCE PROATE)

DT 21-JUL-1886 (REL. 01, CREATED)

DT 21-JUL-1886 (REL. 01, LAST SECURE PROATE)

DE 16 HAYY CHAIN PRECIPEOR REGION (S43)

OC ENTARYOTH, KETANOA, CRORDATA, VERTEBRATA, TETRAPOON, MAND

CETURARY, RODESTIA,

RN 51214548

RN 512 RN 50218VCE FROM N.A.

RY SEQUENCE FROM N.A.

RX HEDLINE; 81214548.

RA BOTHELLA L.M. PARKIND M., RETH M., IMANISHI-KARI T., RAJENSKY K.,

RA BOTHELLA L.M. PARKIND M., RETH M., IMANISHI-KARI T., RAJENSKY K.,

RA BALTIMORE D.;

RC CELL J. 81623-637(1991).

RE CELL J. 81623-637(1991).

RE THE CAMMA-73. CHAIM MENA WAS CLONED FROM A HYBRIDOMA MAKING

CC MITTER CAMMA-73. CHAIM MENA WAS CLONED FROM A HYBRIDOMA MAKING

CC MITTER CAMMA-73. CHAIM MENA WAS CLONED FROM A HYBRIDOMA MAKING

CC MITTER CAMMA-73. CHAIM MENA WAS CLONED FROM A HYBRIDOMA MAKING

CC MITTER CAMMA-73. CHAIM MENA WAS CLONED

RED COUNTY OF THE MATTER (4-HTDROXY-3-NITROPHENYL)ACETYL (NPB

DE MALIN MATTER CAMMA-73.

FIN COMMAIN 10 137 IG HEAVY CHAIN V REGION (543).

FIN COMMAIN 50 69 FRAMEWORK 1.

FIN COMMAIN 50 69 FRAMEWORK 2.

FIN COMMAIN 10 10 117 FRAMEWORK 3.

FIN COMMAIN 118 117 FRAMEWORK 3.

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PREQUENCE FROM N.A.

SEQUENCE FROM N.A.

C. STRAIN-C57BL/6;

X. MEDINEZ B. 1234548.

A. MOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-MARI T., RAJEWSKY K.,

A. MOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-MARI T., RAJEWSKY K.,

A. MALTIMORE D.: 1, 1913.

R. CELLING S. G. CONTROLL M. R. M. M. S. CLOND FROM A HTERIDOM MAKING

CC. L. MITHOLES D. THE MATEN (4-HIDROXY-J-NITROPHENTLANCETTL (NPB

CC. MATTHOLES D.

DR PER, MO2034, MINGSIS.

DR PER, MO2034, MINGSIS.

DR HESP, PO1810. 131ML

REFERENCE FROM TO THE MATEN (4-HIDROXY-J-NITROPHENTLANCETTL (NPB

CR. MO2034, MINGSIS.

DR HESP, PO1810. 131ML

DR H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              effes
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Best Local Similarity 100.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN 123
DISULFID 41
NON_TER 137
SEQUENCE 137 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THO JOSES STANDARD: PRT: 139 AA.
PRO1351 PRO1352: PRT: 139 AA.
13UL-1986 (REL. 01 CREATE)
13 UL-1986 (REL. 01 LAST SEQUENCE UPDATE)
14 ULT-1986 (REL. 04 LAST SEQUENCE UPDATE)
16 HAVY CHAIN PRECURSOR V RESIGN (BI-6 / 186-2).
MIS MICCULG (MOUSE)
MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 SSLTSEDSAVY 113
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FRAMESOR I.
COMPLEMENTARITY-DETERMINING 1.
FRAMESOR Z.
PRAMESOR J.
BROGGENT J.
BROGGENT J.
JH SCORENT.
JH SCORENT.
STAILABRIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 11; DB 1; Length 137;
Pred. No. 1.54e-09;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-836-455-4.rsp
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                                                                                                                                                                                                                                                                                                                                                                                                        å
                                                                                                                                                                                                                                                                                                                    A BALTHOME D.:

1. CELL 74:25-637(1991).

1. CELL 74:25-637(1991).

1. THIS GERMALINE GERGE BELONGS TO A SET OF CLOSELY RELATED GENES

2. T. THIS GERMALINE GERGE BELONG OF NPB ANTIBODIES.

2. T. THIS GERMALINE GERGE VERTICALS OF NPB ANTIBODIES.

2. THE STATE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.2%;
Best Local Similarity 100.0%;
Matches 11; Conservative
                                                                                                                                                                                                                  Query Match 6.5%;
Best Local Similarity 100.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PORTS: PILTI: STANDARD; PRT; 117 AA.
POLTS: PILTI: OI, CREATED)
OI-UU-1986 (REL. OI, CREATED)
OI-UU-1980 (REL. II, LAST SEQUENCE UPDATE)
OI-UV-1990 (REL. II, LAST SEQUENCE UPDATE)
IO HUNY CHAN PRECURSOR V RECION (186-1).
BUS MUSCULIS (MOUSE).
EUMARYON, METARON; CHORDATA, VERTESRATA; TETRAPODA; MAMMALIA;
EUTHERIA, RODENTIA.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 SSLTSEDSAVY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEGUENCE FROM N.A.
STRAINS-CYBL/S:
MEDLINE: 81235-845.
MEDLINE: 81235-845.
MEDLINE: 81235-845.
MEDLINE: 8123-851.
MEDLINE: 8125-857(1981).
MEDLINE
                                   92 DISSSTAYNO 101
92 DISSSTAYNO 101
                                                                                                                                                                                                                  Score 10; DB 1; Length 117;
Pred. No. 3.41e-07;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 11; DB 1; Length 139;
Pred. No. 1.54e-09;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-836-455-4.xap
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RESULT. 19
ID HYOQUOGES STANDARD; PRT; 114 AA.
AC PO1741,006 (REL. 01, CREATED)
DT 21.-UL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21.-UL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21.-UL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 1G HEAVY CHAIN V REGION (ANTI-ARSONATE ANTIBODY).
OS MIS MESCULES (NOUSE).ON (ANTI-ARSONATE ANTIBODY).
OC EUTHARYON, METACON, CHORDATN, VERTEBRATA; ISTRAPODA, MAMALIA;
RE STRAIN-A, CHORDATIA.
RE STRAIN-A, CHORDATIA.
RE STRAIN-A, CHORDATIA.
RE STRAIN-A, LANGUAGE, A.
RE STRAIN-A, LANGUAGE, A.
RE STRAIN-A, LANGUAGE, LANGUAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.5%; Score 10; DB 1; Ler Best Local Similarity 100.0%; Pred. No. 3.41e+07; Matches 10; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECURECE.
MEDLINE: 84182519.
DILDROP R., BOVENS J., SIE
EMBO J. 3:517-521(1984).
PIR: A02040; MHX58.
HSSP; POL772; IFCV.
THOUNGLOBULIN V RECION
THOUNGLOBULIN V REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN 1 98 ' V SEAMENT.
DOMAIN 99 104 D SECHENT.
DOMAIN 105 118 J SECHENT.
DOMAIN 105 118 J SECHENT.
DOMAIN 105 118 J SECHENT.
DOMERT 18 118
SEQUENCE 118 AA; 12934 MH; 2DIDCETT CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TWOL MOUSE STANDARD: PRT: 118 AA.

PG310-3N-1988 (REL 06, CREATED)

O1-AN-1988 (REL 06, LAST ANDORTION UPDATE)

O1-AN-1988 (REL 21, LAST ANDORTION UPDATE)

TO HEMY CHAIR WERGION (AC38 305.12).

MUS MUSCHLUS (MOUSE)

FULL WITCH MOUSENA, CHORDATA; VERTEBRATA; TETRAPODA;

DUTHERIA; ROBENTA.
STACHARCE,
STACHARCE,
STACHARCE,
P9195438.
AEDLINE: 79195438.
CARRA J.D., NISONOFF A.:
J. INGUNOL. 12:279-284(1979).
J. INGUNOL 13:279-284(1979).
-I- ANTIBODY ISOLATED FROM TEN HICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 SLTSEDSAVY 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIEKEVITZ M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BEYREUTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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40 PGZGLEWIG 48 ||:||:|| 60 PGQGLEWIG 68

Query Match 5.9%; Score 9; DB 1; Length 114; Best Local Similarity 88.9%; Pred. No. 5.92e-05; Matches 8; Conservative 1; Mimatches 0; Indels

0

RESULT

WE SECURE: 16277871.

WE SECURE: 16277871.

RA ANTON: -C::157:449-459(1976).

RL BATCH: J. 157:449-459(1976).

RL BEST: POLITIC FROM THE SEROM OF A SINGLE PARBIT.

PRE: 102101; GARBIL.

DR PIR: 02101; GARBIL.

DR PIR: 02101; GARBIL.

PRE: 02101; GARBIL.

RW TEMOREGICEDELTH V RESION.

RW TEMOREGICEDELTH V RESION.

PRE: 02102.

RW TEMOREGICEDELTH V RESION.

PRESCRIPTION.

PRESCRIP

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ID HYA, SANIT
AC PO1877;
AC PO187
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Best Local Similarity 100.0%; Pred. No. 5.92e-05;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUDCLASS. THERE WAS NO HETEROGENEITY IN THE PER, MODOZIA. GINSRAM. BSSP. POLITIZ. LEGY. HESP. POLITIZ. LEGY. HATTARSONATE ANTIBODY. HATTARSONATE ANTIBODY. BOULTER 114 AA: 12555 MN: 1A027FID CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-UTL-1986 (REL. 01, CREATED)
21-UTL-1986 (REL. 01, LAST ANDORATION UPDATE)
21-UTL-1986 (REL. 01, LAST ANDORATION UPDATE)
1G HEAVY CHAIN V-A1 RECOVER (BS-1).
0RKCTOLAGUS CUNICULUS (RABBIT)
5UKKTOLAGUS CUNICULUS (RABBIT)
5UKKTOLAGUS CUNICULUS (RABBIT)
5UKKTOLAGUS LEVINOATHA.
5UKKTOLAGUS LEVINOATHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LQQSGAELV 12
|||||||||
23 LQQSGAELV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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DEB2C7DA CRC32;

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RESULT 25
ID HV15_MOUSE
AC P01759;
DT 21-JUL-1986
DT 21-JUL-1986
DT 01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mon
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Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE SECURINE FROM N.A.

TO STRAINBEALDS N.A.

TO HEDRICE S. M. MIZISEN E.A., KAVALER J.

MATTER A02014, BWASTE S.

MATTER A02014, BWASTE S.

MATTER HESEP: POLSOF: 1175.

MATTER HESEP: POLSOF: 1175.

MATTER A02014, BWASTE S.

MATTER A02014, BWASTER A02014, BWASTE S.

MATTER A02014, BWASTER A0
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Best Local Similarity 100.0%;
Matches 9: Conservative
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P01735;
21-7UL-1986 (REL. 01, CREATED)
21-7UL-1986 (REL. 01, LAST SEQUENCE UPDATE)
10-MAR-1987 (REL. 04, LAST ANDOTATION UPDATE)
17-EZLL RECEPPOR BETA CHAIN PRECURSOR V REGION (8671).
MUS MUSCULUS (MOUSE).
MUS MUSCULUS (MOUSE).
EURAROTA. RECTAZOA: GODRDATA: VERTEBRATA: TETRAPODA: MAMMALIA;
111-METALA: ROSEBTIA.
                                                                                                                                                                                                                                                            102 EDSAVYFCA 110
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108 EDSAVYFCA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 EDSAVYFCA 110
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108 EDSAVYFCA 116
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P08329:
01-JAN-1988 (PEL. 05, CREATED)
01-JAN-1988 (PEL. 05, LAST SEQUENCE UPDATE)
01-JAN-1988 (PEL. 15, LAST SEQUENCE UPDATE)
10-MAR-1992 (PEL. 15), LAST ANNOTATION UPDATE)
11G HEAVY CHAIN V RELIGION (AC38 13:3).
HUS MUSCULUM (MOUSE): MANOALIA: PERTEBRATA: TETRAPODA: MANOALIA:
EMPARYOTA METHEMA: CHORDATA: VERTEBRATA: TETRAPODA: MANOALIA:
111 ENTRERIA: MODERTIA.
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01-JAY-1988 (REL. OS, LAST SEQUENCE UPDATE)
01-WOY-1980 (REL. OS, LAST SEQUENCE UPDATE)
1G HEAVY-CHAIN PRECURSOR V RECTON (VHSS8 AL/AA).
MUS HOSCULJS (MOUSE)
MUS HOSCULJS (MOUSE)
MUSHOVA: METALON; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
MUSHOVA: METALON; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 PGQGLEWIG 68
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60 PGQGLEWIG 68
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(REL. 01, CREATED)
(REL. 01, LAST SEQUENCE UPDATE)
(REL. 17, LAST ANNOTATION UPDATE)
                                                                                                                            STANDARD:
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                                                                                                                                                                                                                                                                                                                                                                     Score 9; DB 1; Length 133;
Pred. No. 5.92e-05;
0; Mismatches 0; Indels
                                                                                                                            . PRT:
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COMPLEMENTATIV-DETERMINING 1.
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BY SIMILARITY.
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V SEGMENT.
J SEGMENT.
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Pred. No. 5.92e-05;
0: Mismatches 0: Indels
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PIR. ADOD J. 3:17-5331304).
PIR. ADODJ: HINSIS.
HISS. POILT: J. IFGY.
DOMAIN PROCESS.
DOMAIN 99 105
DOMAIN 99 105
DOMAIN 106 120
DOMAIN 120 DOMAIN 120 12
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DE RESULT 36

ID HV4 JOUSE STANDARD; PRT; 118 AA.

AC P03980; CPCT-1986 (REL. 02, CREATED)
DT 33-0CT-1986 (REL. 02, CREATED)
DT 33-0CT-1986 (REL. 02, CREATED)
DT 03-0CT-1986 (REL. 03, LAST SEQUENCE UDANE)
DT 01-ACC-1986 (REL. 03, LAST ANDOVATION UPDATE)
DE 104-NC-1982 (REL. 03, LAST ANDOVATION UPDATE)
RE 104-NC-1982 (REL 03, RICHARDS J.E., BLATTHER F.R., MUSHINSKI J.F.
RICHARD ACCOUNTY, ACAD. SCI. U.S.A. 81:4164-4168(1984).
DR PIR. ACCOUNTY, ACAD. SCI. U.S.A. 81:4164-4168(1984).
DR PIR. ACCOUNTY AND SCI. U.S.A. 81:4164-4168(1984).
RESED: P01810; LYHL.
PROC. NATI. ACAD. SCI. U.S.A. 81:4164-4168(1984).
DR PIR. ACCOUNTY AND SCI. U.S.A. 81:4164-4168(1984).
PR PIR. ACCOUNTY AND SC
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RE SECURICE PROM N.A.

RE MANDANE, 8.222.82.

RE KANDANE, 8.222.82.

RE MANDANE, 8.222.82.

RE PROC. MAT. ACAD. SCI U.S.A. 79:2996-3000(1982).

RE PROC. MAT. ACAD. SCI U.S.A. 79:2996-3000(1982).

DR PIR, MOZO42; HYMSSI.

DR PIR, MOZO42; HYMSSI.

DR HESS: POLT99: LITEL.

DR
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Best Local Similarity 100.0%; Pred. No. 5.92e-05;
Matches 9; Conservative 0; Mismatches 0; Indels
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|79 YNQKFKGKA 87
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MUS MUSCULUS (MOUSE).
EUTARYOTA: METAROA; CHORDATA: VERTEBRATA;
EUTHERIA; RODENTIA.
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PO$321, US STANDARD; PRT; 130 AA.

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60 PGQGLEWIG 68
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Pred. No. 5.92e-05;
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IG HEAVY CHAIN V REGION (TEPC 1017) FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1.

SIEKEVITZ M., BEYREUTHER K.,

US-08-836-455-4.rsp

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Mon Apr 19 13:24:00 1999
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SECURNCE B144002

RECHAVI G. RAM D. GLAZER L. EANUT R. GIVOL D.;

PROC. MATL ACAD. SCI. U.A. 80:855-859(1983).

R EMBL. JOOJOL STUBLE.

R PIR ACQCIA STUBLES.

R HESSP. POIDLO: IPTB.

R HESSP. POIDLO: IPTB.

I HEMPROCLOBULIN V REGION: SIGNAL.
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Best Local Similarity 100.0%;
Matches 9; Conservative
                       I NATURE 11236-40(1984)

C I THIS CLORE WAS ISSOLATED FROM A CYTOTOXIC T LYMPROCYTE.

R PIR, ACQUIZ, RWISSS.

R T-CELL. RECEPTOR: SIGNAL.

T SIGNAL 1110

T CHAIN 1110

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Best Local Similarity 100.0%; Pred. No. 7.61e-03:
Matches 8: Conservative 0: Mismatches 0: Indels
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Best Local Similarity 100.0%;
Matches 8; Conservative
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NON_TER 117
SEQUENCE 117 AA;
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RYIB_HUMAN STANDARD: PRT: 117 AA.

PO1743;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1986 (REL. 34, LAST ANFORMATION UPDATE)
01-OCT-1986 (REL. 34, LAST ANFORMATION (RG3)).

RONO SAPIEMS (RUTAN)).
RONO SAPIEMS (RUTAN)).
RONO SAPIEMS (RUTAN).

RUTANDARIA: PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SERVAIN-BALB.B;
STRAIN-BALB.B;
STRAIN-BALB.B;
STRAIN-BALB.B;
SAITO H., KRANZ D.M., TAKAGAKI Y.,
TONFIGANA S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REDILIE: 8839408.
MATSUDA F., LZE K.H., NAKAI S., SATO T., ONNO H., FUUUDARA S., KONDO T.;
EMBO J. 7:1047-1051(1989).
EMBO J. 7:1047-1051(1989).
EMBO J. 70148; - NOT_ANNOTATED_CDS.
PIR: SO0476; HYHU35.
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190138:
21-UL-1986 (REL. 01, CREATED)
21-UL-1986 (REL. 01, LAST EQUURNCE UPDATE)
21-UL-1986 (REL. 01, LAST SQUURNCE UPD
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40 SCKASGYT 47
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MUNOGLOBULIN V REGION; SIGNAL.
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117
117 AA;
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1G HEAVY CHAIR . ...
117
12946 MW; BCC8B1DB CRC32:
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COMPLEMENTARITY DETERMINING 2.
FRAMERORM 3.
COMPLEMENTARITY DETERMINING 3.
FRAMERORM 4.
BY SIMILARITY.
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Pred. No. 7.61e-03;
0; Mismatches 0; Indels 0;
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Pred. No. 5.92e-05;
0; Mismatches 0; Indels
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Best Local Similarity 100.0%;
Matches 8; Conservative
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Best Local Similarity 100.0%;
Matches 8; Conservative
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Best Local Similarity 100.0%;
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P94436:
13-AGC-1987 (REL. O5, CREATED)
13-AGC-1987 (REL. O5, LAST REQUENCE UPDATE)
13-AGC-1987 (REL. O5, LAST REQUENCE UPDATE)
13-AGC-1987 (REL. O5, LAST REQUENCE UPDATE)
13-AGC-1987 (REL. O5, LAST REQUENCE)
13-AGC-1987 (REL. O5, LAST ANNOTATION UPDATE)
13-AGC-1987 (REL. O5, LAST REQUENCE)
13-AGC-1987 (REL. O5, LAST REQUENCE)
13-AGC-1987 (REL. O5, LAST REQUENCE)
13-AGC-1987 (REL. O5, LAST REQUENCE UPDATE)
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40 SCRASGYT 47
                                                                                                                                                                                                                                                                                                     105 DSAVYFCA 112
|||||||
109 DSAVYFCA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLER J. :AGGE W., MELECK
APPLER J. :
ATURE 312:771-775(1984).
VIR: A02010: RWHUAA.
ISSP; P01607; IMCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
EQUENCE: 85086254.
JIM G.K., YAGUE J., NELSON J., MARRACK P., PALMER E., AUGUSTIN A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VOL_CARAD (REL. 16, CREATED)
19.00(190, OREL. 16, CREATED)
1.00V-1990 (REL. 16, LAST SECURENCE UPDATE)
1.0EN-1990 (REL. 17, LAST ANDOTATION UPDATE)
0.HANY CHAIN MERCURSON REGION (3).
1.0EN-1991 (REL. 17, LAST ANDOTATION UPDATE)
1.0EN-1991 (REL. 17, LAST ANDOTATION UPDATES)
1.0EN-1991 (REL 18, LAST ANDOTATION UPDATES)
1.0EN-1991 (REL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISON M.R., MIDDLETON D., MARR G.W.;

OC. NATL. ACAD. SCI. U.S.A. 85:1566-1570(1988)

BL. J0356.6 (21390) -.

BL. A2956. A2956.

SP. PO1772; 2784.

SP. PO1772; 2784.

SP. PO1772; 2784.

SP. PO1772; 2784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECEPTOR: MHC; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117
117 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          אג 131
גא 131,
     (REL. 01, CREATED)
(REL. 01, LAST SEQUENCE UPDATE)
(REL. 30, LAST ANNOTATION UPDATE)
                                                                                                                                                     STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13220 MW; AB59C5F5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IG REAVY CHAIN V REGION (3).
FRANCHORA I.
COMPLEMENTARITY-DETERMINING 1.
FRANCHORA J.
FRANCHORA J.
FRANCHORA J.
FRANCHORA J.
FRANCHORA J.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 8; DB 1; Length 131;
Pred. No. 7.61e-03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 8; DB 1; Length 130;
Pred. No. 7.61e-03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 8; DB 1; Length 117;
Pred. No. 7.61e-03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T-CELL RECEPTOR ALPHA
V SEGMENT.
J SEGMENT.
                                                                                                                                                           PRT;
                                                                                                                                                     135 AA
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US-08-836-455-4

0

0

Caps 0 0.

Gaps

US-08-836-455-4.zsp

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RESULT 33

DE TAZAJUMAN STAKDARD; PRT; 139 AA.

AL DEVAZAJUMAN STAKDARD; PRT; 139 AA.

DE 13-ND-1987 (REL. 05, CREATED)

DE 13-ND-1987 (REL. 05, LAST REQUENCE UPDATE)

DE 15-ND-1987 (REL. 05, LAST REQUENCE UPDATE)

DE 15-ND-1987 (REL. 05, LAST REQUENCE PRDATE)

DE 15-ND-1987 (REL. 05, LAST REQUENCE VERZION (CTL-L17).

OR POWN SAPIRS (RUMAN).

OR EUTHELN; PRIMATES.

OR EUTHELN; PRIMATES.

OR EUTHELN; PRIMATES.

OR EUTHELN; PRIMATES.

RI 151

RN MEDLINE; 8677678, L.). STRONINGER J.L.;

RI 1940000ENDTICS 4. 21.7-21(1985).

OR LEIDEN J.M., PRASER D., STRONINGER J.L.;

RI 19411 SS 23-144, 78.

DE 2011, HASSES; GASPAGG. .

DE 2011, HASSES; GASPAGG. .

DE 2011, HASSES; GASPAGG. .

DE 2011, RECEPTOR RELYCOPROTEIN; SIGNAL.

FOR CHAIN 28 13 27 T-CELL RECEPTOR ALPHA CHAIN V REGION.
                                   PRESULT 36.

ID HV3D, HDMAN STANDARD; PRT; '115 AA.

AC 201765;
DT 21-7UL-1996 (REL. 01, CREATED)

CT 21-7UL-1996 (REL. 01, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                              $ B
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

Best Local Similarity 100.0%;

Matches 7: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apr 19 13:24:00 1999
                                                                                                                                                                                                                                                                                    99 DYWGQGT 105
|||||||
125 DYWGQGT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER 1 1 1
NON_TER 111 111
SEQUENCE 111 AA: 12304 MM; 13340E48 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NATURE 108:145-149(1984).
PIR. A02000; RWHDVT.
HSSP: P01607; ZINN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER 143
SEQUENCE 143 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 DSAVYFCA 112
||||||||
109 DSAVYFCA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 SCKASGYT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE: 84142259.
YANAGI Y., YOSHIKAI Y., LEGGETT
MAK T.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-CELL RECEPTOR BETA CHAIN PRECURSOR V REGION (1735).
HOMO SAPIENS (HUMAN).
EURANIOTA: METAZOA, CHORDATA; VERTEBRATA; TETRAPODA;
EUTHERIA: PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 7; DB 1; Length 111;
Pred. No. 6.73e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::;}.
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Pred. No. 7.61e-03;
O; Mismatches O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-CELL RECEPTOR ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
T-CELL RECEPTOR BETA CHAIN V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4080B85F CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-836-455-4.rsp
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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RESULT. 37

IDENTIFY STANDARD; PRI; 116 AA.
AC P0383; REI, 02, CREATED;
DI 31-0CT-1986 (REL, 02, CREATED)
DI 32-0CT-1986 (REL, 02, CREATED)
DI 32-0CT-1986 (REL, 02, LAST REQUENCE UPDATE)
DI 10-FER-1991 (REL, 01, LAST REQUENCE UPDATE)
DE 10-HEAVE CHAIN PRECURSOR V REGION
CONTRARCONTOS PRANCISCI (HOUN SUARK),
OC CUTANTOSTANDA (GLONG MARK), VERTZERATA; PISCES; GNATHOSTOMATA,
CONTRARCON, METAROA; GRONDATA, VERTZERATA; PISCES; GNATHOSTOMATA,
CONTRARCON, METAROA; GRONDATA, VERTZERATA; PISCES; GNATHOSTOMATA,
RI PROCESSOR N. BERGER L., MURPHY K., LITHAN R., HINDS K.,
RI LITHAN G. N. BERGER L., MURPHY K., LITHAN R., HINDS K.,
RI PROC. NATL. ACAD. SCI. U.S.A. 82:2082-2086(1985).
DR MED. HAL195; GZI.100;
DR MED. HAL195; GZI.100;
DR FIR, ACCOSS; HYRK.
DR HIS PO1789-1 CREJ.
DR FIR, ACCOSS; HYRK.
DR HIS PO1789-1 CREJ.
DR FIR, ACCOSS; HYRK.
DR HIS PO1789-1 CREJ.
DR HIS PO1789-1 LIS IG HEAVY CHAIN V REGION.
DR HIS PO1789-1 LIS IG HEAVY CHAIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14

RESULT 14

RESULT 15

RESULT 16

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BY SEMUCIEN E. T. OTRINSSON S.G.O., VON BAHR-LINDSTROM H.;

RICHARCH E. T. OTRINSSON S.G.O., VON BAHR-LINDSTROM H.;

RICHARCH E. T. OTRINSSON S.G.O., VON BAHR-LINDSTROM H.;

RICHARCH E. T. OTRINSSON S.G.O., VON BAHR-LINDSTROM, (1978).

RICHARCH E. T. OTRINSSON S.G.O., VON BAHR-LINDSTROM, (1978).

RICHARCH E. T. OTRINSSON S.G.O., NAMEZION A MYZIONA, PROTZIN.

RICHARCH E. T. OTRINSSON S.G.O., NAMEZION A MYZIONA, PROTZIN.

RICHARCH S.G.O., VON BAHR-LINDSTROM, PROTZIN.

RICHARCH S.G.O., VON BAHR-LINDSTROM, PROTZIN.

RICHARCH S.G.O., VON BAHR-LINDSTROM, H.;

RICHARCH S.G.O., VON BAHR S.G.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 4.6%; Score 7; DB 1; Length 115; Best Local Similarity 71.4%; Pred. No. 6.73e-01; Matches 5; Conservative 2; Mismatches 0; Indels
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125 DYWGQGT 131
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**RANCA.**-**

**CHEMAN 1.1., PUDENBERG H.H.;

**J. EXIST.**

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**CHEMAN 2.1., PUDENBERG H.H.;

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IG HEAVY CHAIN V-III RECION (TIII).
ROMO SADIENS (HUMAN). RECIONATO: VERTEBRATA; TET
EURANYON, HETALOA. CHORDATA: VERTEBRATA; TET
INTHERIA; PRIMATES.
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MEDLINE, 8105231.
KENTEN J. H. MOLGANAD H.V., HOUGHTON H., DERBYSHIRE R.B., VINTY
BELL L.O., GOULD H.J.;
PROC. NATL. ACAD. SCI. U.S.A. 79:8661-665(1982).
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Pred. No. 7.61e-03;
0; Mismatches 0; Indels
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RESULT 41

ID HYH. HUMAN STANDARD; PRI; 120 AA.

AC 98041; 995 (REL. 32 CREATED)

TO 1.WV-1995 (REL. 32 LAST SEQUENCE UPDATE)

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Query Match
Best Local Similarity 100.01; Pred. No. 6.73e-01; Matches 7: Conservative 0; Mismatches 0; Indels b 21 SCKASOY 27
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Best Local Similarity 100.0%;
Matches 7; Conservative
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WELLINE, 9025598.

ETOPPIN CH. BELLOTI V. NERL A. MERLINI G., GANVER F.,
EUR. J. BICCHEM, 228.886-883(1995).

IMMINOCLOBULIN V. RECOLD

LOUISIER 120 130 13772 Mp., 6004F690 CRC32;

SEQUENCE 120 AA: 13272 Mp., 6004F690 CRC32;
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125 DYWGQGT 131
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P07178;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
10 HEAVY CHAIN V-III RECION (GAL).
HOMO SAPINS (HUMAN)
HOMO SAPINS (HUMAN)
EUTHREDA, PETARGAL CHOSDATA; VERTEBRATA: TETRAPODA; MAMMALIA;
EUTHRETAL; PETARGAL CHOSDATA; VERTEBRATA: TETRAPODA; MAMMALIA;
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RILGERANN M. THE COMPOSITION OF 28-33.

SUBMITTED (JUN-1975) TO THE PIR DATH BANK.

- THIS MC GALLY WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.

PIR HISS MC CHAUCH.

LESP NOISON IRVEL.

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MEDLINE: 75059123.
NATANABE S., BARNIKOL H.U., HORN J., BERTRAM J., HILSCHANN
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 354:1505-1509(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 PGQGLEW 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 7: DB 1: Length 118:
Pred. No. 6.73e-01;
0: Mismatches 0: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mon Apr 19 13:24:00 1999
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P01742;
21-701-1986 (REL. 01, CREATED)
21-701-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-701-1986 (REL. 01, LAST SEQUENCE UPDATE)
10 HEAVY CHAIN V-I REGION (EU).
MONO SAPIZHS (BUDAN);
BUNKHOYA, METNEOA; CHORDATA; VERTEBRATA; TETRAPODA; MANNALIA;
EUTHERIL; PRINANTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 DYWGZGT 116
||||:||
125 DYWGQGT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 PGQGLEW 47
|||||||
60 PGQGLEW 66
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21 SCKASGY 27 ||||||| 40 SCKASGY 46

1777

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DE STATA 43

ID STANL STANDARD; PRT; 122 AA.

AC PO1763;

DT 21-JUL-1986 (REL. O1, CREATED)

DT 21-JUL-1986 (REL. O1, LAST SEQUENCE UPDATE)

DT 21-JUL-1986 (REL. O1, LAST SEQUENCE UPDATE)

DT 21-JUL-1986 (REL. O1, LAST ANNOMATION UPDATE)

DE 16 HARVE CHAIN V-III RGION (TRC).

CE DURANTOTA: METANDA: CERRANTA; VERTEBRATA: TETRAPODA: HAMMALIA:

CE DURANTOTA: HETANDA: CERRANTA; VERTEBRATA: TETRAPODA: HAMMALIA:

REALIZIN H., ALTEWOOT P., RUBAN E., KORTT A., STANCOCIK K.,

RA HILGERANIN N.;

RA HILGERANIN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGUIT 40

ID HY99_MOURE STANDARD: PRT: 118 AA.

AC 901899:
DT 21-7UL-1996 (REL. 01, CREATED)
DT 21-7UL-1996 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-7UL-1996 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-7UL-1996 (REL. 01, LAST SEQUENCE UPDATE)
DE 1G HEAVY CHLIN V REZION (X24).
OS HYS MISCULUS (MOUSE)
OS HYS MISCULUS (MOUSE)
OS HYS MISCULUS (MOUSE)
OS EUTHRIAN, RECHETIAN.
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UL BOCKHAISTER $:1188-1186(1970).

C -1-THE SEQUENCE OF THE CAMMA-1 C REGION OF THIS SECOND OF THE CAMMA-1 C REGION OF THIS SECOND OF THE CAMMA-1 C REGION OF THE CAMMA-1 C
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Best Local Similarity 100.01; Pred. No. 6:73e-01;
Matches 7; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 95.7%; Pred. No. 6.73e-01;
Matches 6; Conservative 1; Mismatches 0; Indels
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PILORENT G., LERMAN D., PUTRAM P.W.:
BIOCHEMISTRY 13:2482-2498(1974).
1- THIS CRAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
BISS. NO2052; ABRUGA.
LEGNOCLOBULIN V REDION.
PROMOCLOBULIN V REDION.
PYRROLIDONE CARBOXYLIC ACID.
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NON_TER 122 122
SEQUENCE 122 AA; 13166 MW; D68B085E CRC32;
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P01769; CREL. 01, CREATED)
21.-UL-1986 (REL. 01, CREATED)
21.-UL-1986 (REL. 01, LAST ESCHENCE UPDATE)
21.-UL-1986 (REL. 01, LAST ESCHENCE UPDATE)
21.-UL-1986 (REL. 01, LAST ENCOTATION UPDATE)
10 HEAVY CHAIN V-III REGION (CA).
BOHO SAPIENS (HUMAN). CHORDATA: VERTEBRATA: TETRAPODA: MANMALIA: EUTHERIA: PETRAFOTA: MANMALIA:
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KEDLINE: 71064024.
CUNNINGHAM B.A., RTIISHAUSER U., GALL
WANDAL M.J., EDELMAN G.M.;
BIOCHEMISTRY 9:3161-3170(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC
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US-08-836-455-4.rsp

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RESULT 44

IN HYS., HUMAN STANDARD: PRT; 126 AA.

AC PAIR, 1366 (REL. 01, CREATED)

DT 21-UTL-1366 (REL. 01, CREATED)

DT 21-UTL-1369 (REL. 01, LAST SEGGENCE UPDATE)

DT 21-UTL-1369 (REL. 21, LAST SEGGENCE UPDATE)

DT 10. HAME-1989 (REL. 21, LAST SEGGENCE UPDATE)

DT 10. HAME-1989 (REL. 21, LAST SEGGENCE UPDATE)

DT 10. HAME-1989 (REL. 21, LAST SEGGENCE UPDATE)

DE 10. HAME-1989 (REL. 21, LAST SEGGENCE UPDATE)

DE 10. HAME-1989 (REL. 21, LAST SEGGENCE UPDATE)

DE 11. HAME-1989 (REL. 21, LAST SEGGENCE UPDATE)

RN 11. HAME-1989 (REL. 21, LAST SEGGENCE UPDATE)

RN SCHEILT W. E., JUNG H. -D., PALM W., HILSCHMANN N.;

RN SCHEILT W. E., JUNG H. -D., PALM W., HILSCHMANN N.;

RN SCHEILT W. E., JUNG H. -D., PALM W., HILSCHMANN N.;

RN SCHEILT W. E., JUNG H. -D., PALM W., HILSCHMANN N.;

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RN SCHEILT W. JUNG H.
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W REDIANO TO 53.
A HOOD L. MARGOLIES H.N., GIVOL D., ZANUT R.,
UNPUDLISHED RESULTS, CITED BY:
L DADLAN E.A. DAVIES D.R., PECHT I., GIVOL D., WRIGHT C.,
L PADLAN E.A. DAVIES D.R., PECHT I., GIVOL D., WRIGHT C.,
L COLD SPRING HAB. STOP. OUNTE. BIOL. 41:627-637(1977).
C ' THIS ALEPHA CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT HAS
C MITI-DINITROPHENIL ACTIVITY.
B PIEL NATIONAL GROUND ACCIVITY.
B PIEL PADLOS ANGESS.
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11-UL-1986 (REL, OL CREATED)

11-UL-1986 (REL, OL CREATED)

11-UL-1986 (REL, 31 LAST ANGONATION UPDATE)

11-FEN-196 (REL, 31 LAST ANGONATION UPDATE)

110 HEAVY CHALM PRECUSSOR V REGION (MOPC 315)

MIS HISCULUS (MOUSE)

MINATOTA: METAGOA: CHORDATA; VERTEBRATA; TETRAPODA; MAI

11 LERIA: RODERTIA.
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Guery Match

Beat Local Similarity 71.4%; Score 7; DB 1; Length 127;

Beat Local Similarity 71.4%; Pred. No. 6.72e-01;

Matches 5; Conservative 2; Hismatches 0; Indels
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MEDILE: 9030531

RINFERT A., BORNE C., DORRINGTON K.J., KL.

NOL. LEGINOL. 36:431-434(1989).

[2] LIGHTHOL. 36:431-434(1989).

[3] LIGHTHOL. 36:431-434(1989).

SECURACE OF 1-13.

ACAD. SCI. U.S.A. 74:5892-589

(1)
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MEDILURE, 79.48789.
GCHECHER 1., MOLF O., ZEMELL R., BU
FED. PROC. 38:1839-1645(1979).
GUIDENIC OF 199-136.
SEQUENCE OF 1470779.
FRANCIS S.H. LESLIE R.G.O., HOOD L.
FRANCIS S.H. LESLIE R.G.O., HOOD L.
FINCE. MATL. ACAD. BCI. U.S.A. 71:111
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|||||||
125 DYWGQGT 131
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MOD_RES 1 1 1
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SEQUENCE 122 AA; 1347
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124 LDYWGQG 130
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               7 REGION; SIGNAL.
18
137 IG
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.; 13472 MW;
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71:1123-1127(1974).
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       HEAVY CHAIN V REGION (MOPC 315)
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                           SECURNCE FROM N. A.
STRAINWALD, MAISS.
STRAINWALD, MAISS.
SHELAND V. D. FLUNKETT G. III. I
GENOMICS 16:551-551(1993).
EMBL. 110328. 020564.
EMBL. 100218. 020564.
EMBL. 100218. 1007113.
EMBL. 100218. 1007111.
EMBCLEME 1156 A. 116633 MH; 5
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p31468;
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SEQUENCE FROM N.A.

SECHANGER J. MITOGRIAN C.A., STEINER L.A.;

SCHWAGER J. STEINER L.A.;
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PROMARYOTA: GRACILICUTES;
ENTEROBACTERIACEAE.
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PROS57;

OL-FEB-1991 (REL. 17, CREATED)

OL-FEB-1991 (REL. 17, LAST SEQUENCE UDDATE)

OL-FEB-1991 (REL. 17, LAST SEQUENCE UDDATE)

OL-FEB-1991 (REL. 17, LAST SEQUENCE UDDATE)

OL-FEB-1991 (REL. 17, LAST SANDOTATION UDDATE)

OL-FEB-1991 (REL. 17, LAST ANNOTATION UDDATE)

OL-FEB-1991 (REL. 17, LAST SEQUENCE UDDATE)
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A; 15080 MY; D8327985 CRC32;
DB 1; Le
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16, LAST SEQUENCE UPDATE)
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COMPLEMENTAL DETERMINING 1
FRAMEWORK 2.

COMPLEMENTAL TOFTERMINING 2
FRAMEWORK 4.

FRAMEWORK 4.

FRAMEWORK 5.

COMPLEMENTAL TOFTERMINING 3

FRAMEWORK 6.

FRAMEWORK 6.

FRAMEWORK 7.

FR
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Pred. No. 6.73e-01;
0; Mismatches 0; Indels
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Pred. No. 6.73e-01;
0; Mismatches 0; In
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                                                                                                  969C1A9E CRC32;
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                                             Length 155;
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   Indels
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W SULT C.J. WHITE O. OLSEN G.J. REDG L. PLESCHMANN R.D.

N STYPIN G.G. BLAKE J.A. FITZEBERLD L.M. CLAYYON R.A. GOCAYNE J.D.

N KERLAYAGE A.R., DOUGHERTY B.A., TOMB J.F. ALMANS M.D., REIGH C.I.,

N OVERBEER R., KIRHESE E.F., WEINSTOCK K.G. MERRICK J.M. GLODEK A.,

SCOTT J.L., GEOGRACEN N.S.M., WEITSHAN J.F., FURRHANN J.F., MOUTEN D.,

N TITZEBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.M., HANNA M.C.,

N COTTON M.D., ROBERTS K.M., HURST M.A., RAIME B.F., BORDOWSK M.,

N CLENK H.F., FRASER C.M., SUTTE H.O., HOESE C.R., VEWER J.C.,

N KLENK H.F., FRASER C.M., SATTE H.O., HOESE C.R., VEWER J.C.,

COLOR DE SHILLARITI TO M.JANNASCELI HUDGOJ.

N TIGH WITCH DE STOTEIN TRANSCERBRANE PROTEIN (POTENTIAL).

M HYDOTHITICAL PROTEIN TRANSCERBRANE
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I CAPALUTIC ACTIVIT: NAD(P)H ACCEPTOR NAD(P)(+) + REDUCED
ACCEPTOR
OFFICER SHAPE PLAYOROFIZIN
OFFICER SHAPE PLAYOROFIZIN
SUBJUNIT: HOMODIMER
OFFICER SHAPE FORECCCIC REDUCARBONS (GOVERNED BY THE AROMAT
INDECEMENTAL BOOKINGS. CTYOFIASMIC.
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YCCA, HETJA STANDARD: PRT: 254 AA.
P81318: 15-JUL-1998 (REL. 36. CREATED)
15-JUL-1998 (REL. 36. LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36. LAST ANYOTATION UPDATE)
15-JUL-1998 (REL. 36. LAST ANYOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIR., BINCHET M.M., TALALAY P., AMEL L.M.,
PROC. MATL. ACAD. SCI. U.S.A. 92:10815(1995).
PROC. TATL. ACAD. SCI. U.S.A. 92:10815(1995).
PROC. TOMETION IT EXEMPTE APPRENENTLY SERVES AS A QUINONE REDUCTAGE IN
CONNECTION WITH CONJUGATION PRACTIONS OF PURPOUTIONS INVOLVED IN
DEPOXICATION WITHAY AS WELL AS IN BIOSETHERIC PROCESSES SUCH AS
THE VITAMIN K-PEPENDENT GAMMA-CARBONIATION OF GLUTAMATIL RESIDUES
THE PROTEROBLY SERVINESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 VFLFLLS 84
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6 VFLFLLS 12
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ISSUE-LYER:
ISSUE-LYER:
I R., 96004635,
I R., BARNEHER M.A., TALALAY P., ANZEL L.M.;
ROC: NATL. ACAD. SCI. U.S.A. 92:8846-8850(1995).
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TRAIN=JAL-1 / DSM 2661 / ATCC 43067;
DDLINE; 96337999.
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HAEBACTERIA; EURYARCHABOTA; METHANOCOCCALES; METHANOCOCCACEAE.
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10 50 POTENTIAL,

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92 112 POTENTIAL,

92 112 POTENTIAL,

133 153 POTENTIAL,

234 AN; 29965 MH; OBJECODD CRC12;
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                  0
117
160
          ACETYLATION.
PE->KK: DESTROY ENZYME ACTIVITY.
V->D: DESTROY ENZYME ACTIVITY.
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                                                                                                                                   ACETYLATION;
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              RH SEQUENCE PROM N.A., AND PARTIAL SEQUENCE.

RH SEQUENCE PROM N.A., AND PARTIAL SEQUENCE.

RH MISSON-LIVER.9737.

RH MISSON-LIVER.9737.

RH MISSON-LIVER.9737.

RH MISSON-LIVER.9737.

RH MISSON-LIVER.9737.

RH MISSON-LIVER.9737.

RH PROTEINS CI. 31.195-1104 (1994).

CC -1- FUNCTION: THE EMBTHE APPAREVILL SERVES AS A QUINONE REDUCTASE IN CONNECTION WITH CONSUMATION EXCITONS OF HYDROQUINONS INVOLVED IN CONTROLICON THE MINING APPAREVILL SERVES AS A QUINONE REDUCTASE IN CONTROLICON BY PARTIAL ASSONANTION OF CULTUMANTIL RESIDUES AS THE VIZIALIE ASSONANTIL RESIDUES CONTROLICON CONT
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Best Local Similarity 100.0%;
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DROU_PAT

POSSES 1054/19;

LAGT SCOURAGE UPDATE)

11 - THE - 199 (FEEL . 9) - CREATED)

12 - THE - 199 (FEEL . 9) - LAGT SCOURAGE UPDATE)

13 - THE - 199 (FEEL . 9) - LAGT SCOURAGE UPDATE)

14 - THE - 199 (FEEL . 9) - LAGT SCOURAGE UPDATE)

DAPPORAGE (CENTROUTASE) (PHYLLOQUINOUS REDUCTASE) (MENAJONE

DAPPORAGE) (ASOREDUCTASE) (PHYLLOQUINOUS REDUCTASE) (MENAJONE
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10 LLSITTG 16
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046459 04058 STANDARD; PRT; 273 AA.

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CONFLICT 134
SEQUENCE 273 AA;
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MEDLINE: 9030194.

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CHEN S.;

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TISSUE-LIVER,
REDILINE, 07057224.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEGUENCE PROM N.A.
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WASILIOU V, TREUBER M.J., POCA A., REUTER S.F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REDIINE: 89062419.
HEDLINE: 89062419.
ANIU M., TUAN H., CHEN S., IYANAGI T., LEE T.D.,
IICCHEMISTRY 27:6877-6883(1988).
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PECLES-BAT:
BELLIES, 88113903.
ANNEY R.M., PICKETT C.B.;
MCH. BIOCHEM. BIOPRIS. 260:847-850(1988).
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OBERTSON J.A., NEBERT D.W., HANKINSON O.;
NEM. SCR. 27:83-87(1987).
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ISSUE=LIVER;
EDLINE; 90094356.
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NYMEY R.M., RODKEY J.A., BENNETT C.D., LO A.Y.H.,
BIOL. CHEM. 262:572-575(1987).
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Itus norvegicus (bāt).
Kartota; Ketasoa; Chordata; Vertebrata; Tetrapoda;
Theria; Rodentia.
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134 K
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US-08-836-455-4.rsp

Page 58

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PICKETT

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2 dbs
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SW: HV02_MOUSE
SW: HV03_MOUSE
SW: HV05_MOUSE
SW: HV05_MOUSE
SW: HV04_MOUSE
SW: HV04_MOUSE
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SW: HV16_HUMAN
SW: HV26_RABIT
SW: HV26_RABIT
SW: HV38_MOUSE
SW: HV16_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROMIG of: /home/obryen/ree455/olig/US08836455.pep sequence 4, application us/08836455 general information:
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SWISS-PROT, Release 36.0, Released on
SPTREMBL, Release 8.0, Released on
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applicant: foon, kenneth a.
applicant: chatterjee, sunil k.
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# Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U. Distribution rights by Oxford Molecular Ltd

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SENES FOR CORE, ENVELO
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       RESULT 2

RESULT 2

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DE COLOR PRELIMINARY: PRT: 118 AA.

AD 002000; PRELIMINARY: PRT: 118 AA.

DE COLOR 1997 (TREMBLEEL. 04, LAST SEQUENCE UPDATE)
DE COLOR 1998 (TREMBLEEL. 04, LAST SEQUENCE UPDATE)
DE COLOR 1998 (TREMBLEEL. 05, LAST ANNOTATION UPDATE)
DE COLOR 1998 (TRAMBLEEL. 05, LAST ANNOTATION UPDATE)
OC UNCLASSIPIZED.

RE 110

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Best Local Similarity 100.0%; Peedt. No. 2.08-20;
Matches 15: Conservative 0: Hamatches 0: Indels
                                                                                                                      ENDIRICE FROM N.A.
STRAITH (NERSHEN) I NOUSE: TISSUE-SPLEEN;
STRAITH (NERSHEN) I NOUSE: TISSUE-SPLEEN;
SPATIALE-BROOMED B: 7 DEMBI/GENBANK/DDBJ DATA BANKS.
DEBI: U44955 (16314);
DEBI: U44955 (16314);
DEBI: U44955 (16314);
DEBI: U44955 (16314);
DEBI: U4495 (1631
NON_TER 1 1 1 1 NON_TER 118 118 118 SEQUENCE 118 AA; 12937 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D44924; G1763745; -.
PPAM; PPOO047; ig.
NON.TER 1 1 1
NON.TER 118 118
SEQUENCE 118 AA; 13117 MM;
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Outry Match 92%; Score 14; DB 11; Length 120; Best Local Similarity 100; 04; Pred, No. 1.10e-17; Matches 14; Conservative 0; Himatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                  Apr
                                                                            D SEQUENCE FROM N.A.

X MENDAN N. SOSSESSAN N. TRANSOTO M., SAKIHAMA T.,

REMONAN N. MANDHITANA N.,

LUNDAN N. MANDHITANA N.,

HTBERDOMA 14.521-526(1995).

R EMEL. SEBST, GABSSSSS.

R FPAM. PFO0047, 19.

SEQUENCE 110 AA: 11147 MM; 3EA54DBB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                            19 13:24:01
                                                                                                                                                                                                                                                                                     S MUSCULUS (MOUSE).
KARYOTA: METALOA; CHORDATA; VERTEBRATA;
THERIA: RODENTIA.
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ID 997746; PRELIMINARY; PRT; 120 AA.

AC 997746; OT 01-MAY-1997 (TREGULERL 03, CREATE)

DT 01-MAY-1997 (TREGULERL 03, LAST SEQUENCE UPDATE)

DT 01-MAY-1997 (TREGULERL 06, LAST NEOTING UPDATE)

DT 01-MAY-1997 (TREGULERL 06, LAST NEOTING UPDATE)

DT 01-MAY-1997 (TREGULERL 06, LAST NEOTING UPDATE)
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Query Match 9.2%; Score 14; DB 11; Le Best Local Similarity 100.0%; Pred. No. 1.10e-17; Matches 14; Conservative 0; Mismatches 0;

Length 118;

Indels

0

Gaps

Page

RESULT 1

ID 009199 PRELIMINARY: PRT: 118 AA.
AC 009199 PRELIMINARY: PRT: 118 AA.
AC 009199 PRELIMINARY: PRT: 118 AA.
DT 01-JUL-1997 (TREDBLEEL, 04, CREATED)
DT 01-JUL-1997 (TREDBLEEL, 04, LAST SEQUENCE UPDATE)
DE 10H MEANT CHAIM (FRANCHEMT)
OC UNKLOMEN.
OC UNKLOMEN.
OC UNKLOMEN.
AC STALIC-ROOALD B:
RN 111
RN 111
RN 1212-ROOALD B:
AC STALIC-ROOALD B:
AC STALIC-ROO

SEÓVENCE FROM N.A. STRAIN-(RESHEW)PI HOUSE: TISSUE-SPIZEN; PAYELLE-BROGARD B.; SUBMITTED (JAN-1896) TO EMBL/GENBANK/DOBJ DATA

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RESULT 6

ID 070568) PRELIMINARY: P)
AC 070568) PRELIMINARY: D)
D1 0.400-1998 (TREMBLEEL 07, CRE
D1 0.400-1998 (TREMBLEEL 07, LAS
D2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ş
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Best Local Similarity 100.0%;
Matches 13; Conservative
SEQUENCE FROM N.A.
STRAIN-BALB/C;
HAWLISCH H., FRANK R., HENNECKE M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P97407 PREZMINANY; PRT; 111 AA.
P97407 PREZMINANY; PRT; 111 AA.
P97407 PREZMINANY; PRT; 111 AA.
O1-MAY-1997 (TREMELREL. O3, CREATED)
O1-MAY-1997 (TREMELREL. O3, LAST SEQUENCE UPDATE)
O1-MOY-1997 (TREMELREL. O5, LAST SEQUENCE UPDATE)
O1-MOY-1997 (TREMELREL.)
O1-MOY-1997 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 13; DB 11; Le
Pred. No. 5.13e-15;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AA
                                                                                                                                                                                                                                                                                                                                                                TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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RESULT
1 P70173 PRELIMINARY: PRT: 138 AA.
1 P70173 PRELIMINARY: PRT: 138 AA.
1 P70173 PRELIMINARY: PRT: 138 AA.
2 PRE-1997 (TREMBLEEL: 02, CARATED)
2 PRE-1997 (TREMBLEEL: 03, LAST SEQUENCE UPDATE)
2 PRE-1997 (TREMBLEEL: 04, LAST SEQUENCE UPDATE)
2 PRE-1997 (TREMBLEEL: 05, LAST SEQUENCE UPDATE)
2 PRE-1998 (TREMBLEEL: 06, LAST ANNOTATION UPDATE)
2 PRE-1998 (MOSED)
3 PRE-1998 (MOSED)
4 PRE-1998 (MOSED)
4 PRE-1998 (MOSED)
5 PRE-199

Overy Match 9.2%; Score 14: DB 11; Le Best Local Similarity 100.0%; Pred. No. 1.10e-17; Matches 14: Conservative 0; Mismatches 0;

Length 138; Indels 0;

Gaps

SOHNS

B., ARSENIEV L.

SICUAL 1 19 POTENTIAL.
CHAIR 20 >138 ONTO HEAVY CHAIR V
NOW THE 138 138 ONTO HEAVY CHAIR V
NOW THE 138 AA: 15848 MF; 75D6DDOA CRC32;

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REAL STATE OF STATE O **8** 8 STEERS Query Match 8.5%; Best Local Similarity 100.0%; Matches 13; Conservative 108 DYWCQGTSVTVSS 120 ||||||||||||||| 125 DYWGQGTSVTVSS 137 Score 13: DB 11: Length 121 Pred. No. 5.13e-15; 0: Mismatches 0: Indels Length 121; ő

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C61250 PRELIMINARY: PRT: 152 AA.
051359.
01.1007-1306 (TREDSLEEL 01. CREATED)
01.0007-1306 (TREDSLEEL 01. LAST SCOURMES UPDATE)
01.7007-1306 (TREDSLEEL 06. LAST ANNOTATION UPDATE)
ANTICER, 9 CELL ARECTOR PRECURSOR.
101.4008-101. RAIN-BALB/C;

STEALINE 96134009. K., HETLIGEN H., RAUS J., VANDEVYVER C.;
THIRROWS, S., MOTHANS K., HETLIGEN H., RAUS J., VANDEVYVER C.;
INGUNOCHMETICS 43:167-168(1396).
EMBL; L43567; G89971; -.
PFAM: PP00047; 49.

SIGNAL 1 19 POTENTIAL.
CHAIN 20 152 ANTICEN, B-CELL RECEPTOR SEQUENCE 152 AA; 16517 MF; A83E9253 CRC32;

Query Match 8.5%; Best Local Similarity 100.0%; Matches 13; Conservative Score 13; DB 11; Length 152; Pred. No. 5.13e-15; 0; Mismatches 0; Indels 0; Gaps ö

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RESULT 8 ID 035842 PRELIMINARY: PRT; 262 \$

Apr 19 13:24:01 Query Match 7.8%; Best Local Similarity 100.0%; Matches 12; Conservative Score 12: DB 11: Length 134; Pred. No. 2.06e-12; 0; Mismatches 0; Indels 0; US-08-836-455-4.rspt Caps

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RESULT 10

DROUGH OF PRELIMINARY: PRT: 243 AA.

AC 035140; PRELIMINARY: PRT: 243 AA.

AC 035140; PREMINERY: 05. CREATED)

DT 01-JAN-1998 (FREMENERY: 05. LAST SEQUENCE UPDATE)

DT 01-JAN-1998 (FREMENERY: 05. LAST SEQUENCE UPDATE)

DO ANTI-CD10 MOAB KI-4 SCFV (FRAMHENY).

OR EUKARYOTA. METAZOA. CORDANYA: VERTERRATA: TETRAPODA: MAMMALIA:

OR EUKARYOTA. MATCH 5. MATTHEY B. LEMKE H., ARENDS J.W., DIEHL V.,

RA KLIMKA A., DARTH 5. MATTHEY B. LEMKE H., ARENDS J.W., DIEHL V.,

RA MOOGRADIO (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

DR MED HAND (AG 1-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

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DR MED HAND (AG 1-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

DR MED HAND (AG 1-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

DR SEQUENCE 243 AA: 2625 Mg. EDAD5383 CRC32:

ENURNCE FROM N.M. MATHET B., LEMKE H., ARENDS J.W., DIEHL V.,
ILLMMA. N. BARTH S., MATHET B., LEMKE H., ARENDS J.W., DIEHL V.,
HOCGENGOM H. REGERT A. DEBLYGENBANK/DDBJ DATA BANKS.
SUBMITTED (NAT. 1997) TO SEBLYGENBANK/DDBJ DATA BANKS.
FRAM: PRO02142; 02390774;
FRAM: PRO02143, 1393
FRAM: PRO02143, 143
1091/TER 243 243
SEGUENCE 243 AA: 26225 May: EOAD5383 CRC32:

8 Ouery Match 7.2h; Score 11; DB 11; Length 243; Best Local Similarity 100.0h; Pred. No. 6.97e-10; Matches 11; Conservative 0; Mismatches 0; Indels 0; Caps 0

RESULT 11

ID 055114 AC 056114 AC 05

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Query Match 6.5%; Best Local Similarity 100.0%; Matches 10; Conservative Score 10; DB 11; Length 37; Pred. No. 1.92e-07; 0; Mismatches 0; Indels 0 Gaps

õ 24 SLTSEDSAVY 33 |||||||||| 104 SLTSEDSAVY 113

DUZ 12

PRELIMINARY; PRT: 98 AA.

1311

PRELIMINARY; PRT: 98 AA.

1311

01-UNI-198 (TREMBLEEL. 06, CREATE)

01-UNI-198 (TREMBLEEL. 06, LAST RECOVENCE UPDATE)

01-UNI-198 (TREMBLEEL. 06, LAST RECOVENCE UPDATE)

01-UNI-198 (TREMBLEEL. 06, LAST RECOVENCE UPDATE)

104 AND PRACESTI

REGULUS (MODERT)

BUSINESTIA, RODENTIA.

11 PRINTOTAL RETALON; CHORDATA; VERTERRATA: TETRAPODA; NAMMALIA:

EUTHERIA, RODENTIA.

11

STOURNOE FROM N.A.
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Ouery Match 6.5%; Score 10; DB 11; Length 98; Best Local Similarity 90.9%; Pred. No. 1.92e-07; Matches 1; Indels Matches 10; Conservative 0; Mismatches 1; Indels 0 Gaps

SEQUENCE 98 AA; 10865 NW; 4C615AE9 CRC32;

103 SSLTSEDSAVY 94

RESULT

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015484;
01-JAN-1998 (TREMBLEEL 05, CREATED)
01-JAN-1998 (TREMBLEEL 05, LAST ESCURNCE UPDATE)
01-JAN-1998 (TREMBLEEL 05, LAST ENCORPTION UPDATE)
01-ANG-1998 (TREMBLEEL 05, LAST ANOCATION UPDATE)
MOR HUSCULUS (MOUSE TRANSCRIPTASE SINGLE-CHAIN VARIABLE FRAGMENT.
MUSKHOTA: METALOA: CHORDATA: VERTEBRATA: TETRAPODA: HAMMALIA:
EUTHERIA: RODENTIA.
(1)

SEQUENCE PROM N.A.

TISSUE-WINSHIDOM.

MEDLINE, 96211469

SHAMEEN F. DUNN I., BAGASRA O., POMERANT.

J. VIRGI., 70.1992-3400(1996).

REDI. (48715; G2289026;

PENM: PFO047; 32

PENM: PFO047; 32

PENM: PFO047; 32

SEQUENCE 263 AA: 27842 NF; AF24DBF6 CRC32; BAGASRA O., POMERANTZ

Query Match 8.5%; Score 13: DB 11: Length 262; Best Local Similarity 100.0%; Pred. No. 5.18\*15; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps

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061552 PRELIMINARY, PRT; 134 AA.
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SENGUENCE FROM N.A. MASHMIRI S.V.S., MILENIC D., CALVO B., ABERGEL C., PALLAN S.A., MASHMIRI S.V.S., MILENIC D., CALVO B., ABERGEL C., PALLAN S.A., MASHMIRI S.V.S., MILENIC D., CALVO B., CEMILA SELLAND, J. SENGL, MASSASSIS, G.193117; - SENGL, MASSASSIS, G.193117; - SENGL, MASSASSIS, G.193117; 49.

SIGNAL 1 19 POTENTIAL.

1 19 POTENTIAL. 20 >134 CC49 PAB. 134 134 134 TEBO7046 CRC32:

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01-AM-1998 (TREMELREL, OS, CREATED)
01-AM-1998 (TREMELREL, OS, LAST SEQUENCE UPDATE)
01-AM-1998 (TREMELREL, OS, LAST SEQUENCE UPDATE)
ANTI-ACID PHOSPHATASE VARIABLE HEAVY CHAIN 18 (FRAGHEÑT).
NUS MUSCULUS (MOUSE)
US MUSCULUS (MOUSE)
TOTHERAIA: ROCHETIA.
TOTHERAIA: ROCHETIA. PRELIMINARY; PRT; 116 AA.

STATES REPORTED TO SERVICE OF THE SE

SEQUENCE FROM N.A.

STOALNESALD/C:
TAKATA R. MITAMOTO Y., HONJOH K., SOEDA T., SAKAMOTO J., MITAMOTO T.,
RATAMO S.,
SUBMITTED (ADR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL. D501,37; D1024480: FYAM. PF000471, 49.

11.
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Ouery Match 6.5%; Score 10; DB 11; Length 116; Best Local Similarity 100 0%; Pred No. 129c-0; Length 116; Matches 10; Conservative 0; Mismatches 0; Indels NON\_TER 116 116 SEQUENCE 116 AA; 13097 MW;

BEFF6ELA CRC32;

0

Gaps

γo 8

RESULT 14

DO 03538: PRELIMINARY: PRT: 120 AA.
AC 03558: PRELIMINARY: PRT: 120 AA.
AC 03558: PRELIMINARY: PRT: 120 AA.
AC 03558: PRELIMINARY: PRT: 120 AC.
DT 01-JAN-1998 (TREDBLEEL: 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREDBLEEL: 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREDBLEEL: 05, LAST SEQUENCE UPDATE)
DE ANTI-ACID PROSPHATASE VARIABLE LIGHT CRAIN 11 (PRAGMENT).
OC EUTHERITA: RODERITA.
CC EUTHERITA: RODERITA.
RE STRAINERITA: PROSPECTION OF REAL PROSPECTION OF RE

MINAMOTO T.

120 AA; 120 k; 13235 MW;

Apr 19 13:24:01

SEQUENCE FROM N.A.

100 T. HIFFORD E. ISHIMARU M., MORIMARA F., ITOH

1 FERMENT. BOCEMG 83:33:340(1997).

EMBL. D6560: B1024549;

100 M.TER 15 15

SEQUENCE 125 AA: 13544 MM; E5389DOD CRC32:

125 13544 MW; E53B9D00 CRC32;

Query Match

Best Local Similarity 100.0%;

Matches 10; Conservative Score 10; DB 11; Pred. No. 1.92e-07; 0; Mismatches ( <u>.</u> Length 249; Indels 0; Gaps

4 LQQSGAELVR 13

EUTHERIA: RODENTIA.

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STARRENC

Query Match
Best Local Similarity 100.0%;
Matches 10; Conservative

Score 10; DB 11; Length 125; Pred. No. 1.92e-07; O; Mismatches 0; Indels 0;

Gaps

ZUR NIEDEN U., FIEDLER U., WEILER E.W.,

0

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23 LQQSGAELVR 32

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RESULT 18

PRELIMINARY, PRT: 133 AA.

AD 03178, PRELIMINARY, PRT: 133 AA.

AD 03178, PRELIMINARY, PRT: 133 AA.

DT 01.90V-1996 (PREMILEEL 01, CREATED)

DT 01.90V-1996 (PREMILEEL 01, LAST SEQUENCE UPDATE)

DT 01.90V-1996 (PREMILEEL 01, LAST SEQUENCE UPDATE)

DE (H-2D, PREMILES 11 I A-BETA MENU.

DE (H-2D, 5 PEM, PREMILONA N. 33 CC2 PRECUISOR (PRADEEMY).

OC EDITARYON, RETAKAN. CROEDATA: TETRAPODA: HAMMALIA:

RE HAMBERT 1. PRAMEER 1. PRAMEER 1. PRAMEER A. TILLINGHAST J.

RA CHOU H.S. WHITELEY D.J. MAPP J.A., PIERCE C.W., SHEVACH E.M.,

RI LOH D.Y.;

RA LOH D.Y.;

RA LOH D.Y.;

RA LOH D.Y.;

RA LOH D.Y.;

RE SEQUENCE 133 AA; 15124 MW; 51D600EF CRC32;

RY SECURICE FROM N.

RY MEDICIES 730-053.

RX MEDICIES 730-053.

RA SPIRZLA D.G. HENNEN I.H., WALSH W.D., BEHLKE M.A., TILLINGHAST J.P.,

RA CHOM H.S., WHITELEF D.J., KAPP J.A., PIERCE C.W., SHEYACH E.M.,

RA LOH D.Y.; MHITELEF D.J., KAPP J.A., PIERCE C.W., SHEYACH E.M.,

RA LOH D.Y.; 138:1991-1995(1987).

RL J. IMPUNC., 138:1991-1995(1987).

RL J. IMPUNC., 138:1991-1995(1987).

RE PERM: PROGONO, 19.

PT SECHAL, MEC.

1 19 POTENTIAL.

PT SECHAL

1 131 NO. 11114 NW: 51D600EF CRC12;

Query Match 5.9%;
Best Local Similarity 100.0%;
Matches 9; Conservative

Score 9; DB 7; Length 133; Pred. No. 4.12e-05; 0; Mismatches 0; Indels Indels 0 Gaps

B 101 EDSAVYFCA 109

RESULT 19
ID 041322 PRELIMINARY; PRT: 98 AA.
AC 041322 PRELIMINARY; PRT: 98 AA.
AC 041322 PRELIMINARY; PRT: 98 AA.
DT 01-UN-1998 (TREMBLER: 05 LAST SEQUENCE UPDATE)
DT 01-UN-1998 (TREMBLER: 05 LAST SEQUENCE UPDATE)
DT 01-UN-1998 (TREMBLER: 05 LAST SEQUENCE UPDATE)
DE RIEDMANDLE PCOM R.
OC EUTHRICH, METHADA, GROEDATH; VERTEBRATA: TETRAPODA; M.
RY SEQUENCE PROM N.A.
RA BORRETZEN M., NATVIG J.B., THOMPSON K.M.;

VERTEBRATA; TETRAPODA; MAMMALIA;

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Query Match 6.5%; Best Local Similarity 100.0%; Matches 10; Conservative 85 SLTSEDSAVY 94 ||||||||| 104 SLTSEDSAVY 113 Score 10; DB 11; Length 120; Pred. No. 1.92e-07; 0; Mismatches 0; Indels 0;

Gaps

0

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MES MUSCULUS (MOUSE). EURANYOTA, METAROA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; ETTHERIA; RODENTIA.

STRAIN-CHAIGE FROM N.A. PIPPEN A.M.M., PISETSKY D.S., WINCOH M.K., ALEXANDER A.L., PIPPEN A.M.M., PISETSKY D.S., GILKESON G.S., CHARLESON G.S.

Query Match 6.5%; Best Local Similarity 100.0%; Matches 10; Conservative Score 10; DB 11; Length 123; Pred. No. 1.92e-07; 0; Mismatches 0; Indels 0 Gaps 0

85 SLISEDSAVY 94 |||||||||| 104 SLISEDSAVY 113

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RESULT 16

RESULT 16

C 054733 PRELIMINARY; PRT; 125 AA.

C 01.-UN-1998 (TREMBLER, 06, LAST REQUENCE UPDATE)

DT 01.-UN-1998 (TREMBLER, 06, LAST ANDOTATION UPDATE)

DT 04.-UN-1998 (TREMBLER, 06)

EMAN 15 HEAVY CHAIN (PRACHENT).

OS NUS MEGILIAS (MODES)

OS RUARYOTA: METAKOA; CHORDATA; VERTERRATA; TETRAPODA.

CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

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PLATELET MEMBRANE GLYCOPROTEIN IB (GPIB) SPECIFIC ANTIBODY (FRAGHENT). 1900: 1900: Sapiens (Human). 1900: Sapiens (Human). 1900: Sapiens (Human). 1901: Sapiens (Human).

SHABE MOL. IMMUNOL. 0:0-0(1997).
EXSL; AF035786; G2668850; -.
NOW\_TER 1 1
NOW\_TER 98 98
SEQUENCE 98 AA; 10912 MM;

Query Match
Best Local Similarity 100.0%;
Matches 8: Conservative 4F9C1186 CRC32;

Score 8; DB 4; Length 98; Pred. No. 6.54e-03; 0; Mismatches 0; Indels 0 Gaps

0

SEQUENCE FROM N A. MEDLINE; 91370594. HIRAIWA A., NUGENT D.J., MILNER AUTOIMMUNITY 8:107-113(1990).

21 SCRASGYT 28 |||||||| 40 SCRASGYT 47

FRANCE SERVICE 
117 20
0992A PRELIMINARY; PRT; 124 AA.
0992A; PREMIMENE; PRT; 124 AA.
0992A; PREMIMER; O3, CREATED)
01-MAY-1997 (TREMELEEL 03, CREATED)
01-MAY-1997 (TREMELEEL 05, LAST SEQUENCE UPDATE)
01-UNY-1997 (TREMELEEL 05, LAST SEQUENCE UPDATE)
01-UNY-1997 (TREMELEEL 05, LAST SEQUENCE UPDATE)
101-MAY-1997 (TREMELEEL 05, LAST SEQUENCE UPDATE)
101-MAY-1997 (TREMELEEL 05, LAST MANOCATION UPDATE)
101-MAY-1997 (TREMELEEL 05, LAST MAYOTATE)
101-MAY-1997 (TREMELEEL 05, LAST SEQUENCE UPDATE)
101-MAY-1997 (TREMELEEL 05, CREATED)
101-MAY-1997 (TREMEL 05, CREATED)
101-MAY-1997 (TREMELEEL 05, CREATED)
101-MAY-1997 (TREMELEEL 05, CREATED)
101-MAY-1997 (TREMELEEL 05, CR

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Ol-NOV-1996 (TREMBLEEL OL CREATED)
OL-NOV-1996 (TREMBLEEL OL LAST SEQUENCE OPDATE)
OL-TWN-1996 (TREMBLEEL OL LAST SEQUENCE OPDATE)
ANG CLASS II I-A-ALPEA MRNA.
(H-2B), 5' END HTREIDOMA AT 3.67 PRECURSOR (FRACKENT).
MUS MUSCULUS (MOUSE).
EURANGOTA, METALAGA, CHORDATA, VERTERBATA; TETRAPODA; HAMMALIA;
EURANGOTA, METALAGA, CHORDATA, VERTERBATA; TETRAPODA; HAMMALIA;
INTERBATA; RODENTIA.

SPOURNE FROM N.A.
SPINELA D.G. 24053.
SPINELA D.G. 14054.
CROD H.S., WHITELET P.J., KADP J.A., PIERCE C.W., SHEYACH E.K.,
LOND.H.S., WHITELET P.J., KADP J.A., PIERCE C.W., SHEYACH E.K.,
LOND.H.S., WHITELET P.J., KADP J.A., PIERCE C.W., SHEYACH E.K.,
LOND.H.S.

J. IMMUNOL. 138:3991-3995(1987). EMBL: M16678; G199460; -. PFAM: PF00047; 1g. SIGNAL: MHC. 1 19 POT SIGNAL: MHC. 1 19 POT

POTENTIAL

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21 SCKASGYT 28 | | | | | | | | | 40 SCKASGYT 47

PRELIMINARY;

132 AA

Query Match 25,28; Score 8: DB 4; Length 125; Best Local Similarity 100.0%; Pred. No. 6.54e-09; Matches 6; Conservative 0; Mismatches 0; Indels

0

Query Match 5.2%; Best Local Similarity 100.0%; Matches 8; Conservative 106 LDYWGQGT 113 |||||||| 124 LDYWGQGT 131 Score 8: DB 4: Length 124; Pred. No. 5.54e-03; 0: Mismatches 0: Indels 0; Indels 0 Gaps

0

B

RESULT 21
ID 099846 PRELIMINARY:
AC 099846;
DT 01-MAY-1997 (TREMBLREEL 03,
DT 01-MAY-1997 (TREMBLREEL 06, CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE) PRT; 125 AA.

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CHAIN 20 >132 POTENTIAL.
NON\_TER 132 132
SEQUENCE 132 AA; 14674 MW; 9364DD4D CRC32;

Query Match 5.2%; Best Local Similarity 100.0%; Matches 8; Conservative Score 8: DB 7: Length 132: Pred. No. 6.54e-03; 0: Mismatches 0: Indels 0

B 103 DSAVYFCA 110 ||||||| 109 DSAVYFCA 116

SECURACE FROM N.A. YI K.S., SUH P.G., RYU S.H., CHOI S.J., KIM H.J., CHUNG J.H., LEE S.D., YI K.S., SUH P.G., RYU S.H., CHOI S.J., KIM H.J., SUBATITED (FEB.-1997) TO EMBL/GENBANK/DDSJ DATA BANKS.
EMBL: UBBO67; G.185548; ...
FFAM: PFOOD-17, LS.

B Query Match 5.2%; Best Local Similarity 100.0%; Matches 8: Conservative 21 SCKASGYT 28 ||||||||| | 40 SCKASGYT 47 Score 8: DB 11; Length 241; Pred. No. 6.54e-03; 0; Mismatches 0: Indels ő Caps 0

REGULT 24

ID 000288 PRELIMINARY; PRT: 244 AA.

AC 000288; OCT 01.597 (TREMELREL. 04, CREATED)

DT 01.5UL-1997 (TREMELREL. 04, LAST SEQUENCE UPDATE)

DT 01.4UG-1996 (TREMELREL. 07, LAST ANOTATION UPDATE)

EXECUTION OF PRACHEM (TRACHEM)

CH SECTY.

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Gaps 0

RESULT 23

PRELIMINARY: PRT; 241 AA.

ID 997771

PRELIMINARY: PRT; 241 AA.

OF 97771

OF 01-4AY-1997 (TREMBLEEL 03, CREATED)

OF 01-4AY-1997 (TREMBLEEL 04, LAST STOURNES PRAKTE)

OF 01-4AY-1997 (TREMBLEEL 04, LAST STOURNES PRAKTE)

OF 01-4AY-1997 (TREMBLEEL 04, LAST STOURNES PRAKTE)

DE NOTE 1997 (TREMBLEEL 04, LAST STOURNES PRAKTE)

OR MIS MONGEN, PREMANIAN PY PRACHEST (TRAMBENT)

OR WITHOUGH AND CHORDATH, VERTEBRATA; TETRAPODA; MANGALTA;

OR WITHOUGH AND CHORDATH, VERTEBRATA; TETRAPODA; MANGALTA;

OR WITHOUGH AND CHORDATH, VERTEBRATA; TETRAPODA; MANGALTA;

RA KIMI J., CROIL H., CHUNG H.K.; SUH P.G., RYU S.H., CHOI S.J., KIM H.

RA KIMI J., CROIL H., CHUNG H.K.;

SUBMITTEED (FEB-1997) TO EMBL/GENBANK/DD5J DATA BANKS.

DR PRAKI, PROGAT; 19
FT NOWL-TER 141 241

FT NOWL-TER 241 241

FT NOWL-TER 241 241

FT STOUR STOURNESS PROGRAM; PROGAT; BEBEZD29D CRC12:

241 ; 26086 MW; EBB2D29D CRC32;

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HOMO SAPIENS (HUMAN). EULARYOTA: METALOA: CHORDATA: VERTEBRATA; EUTHERIA: PRIMATES. [1] TETRAPODA; MAMMALIA;

NON\_TER 244 SEQUENCE 244 AA; SECURNCE PROM N. N. NING M.G., WINTER G.;
NAT. BIOTECHNOL. 15:629-631(1997).
EMBL, V13057; E31575; -.
EMBL, V13057; E31575; -.
FRAM, P\$00047; 19.
NON\_TER 1.

2222222222222

Query March 5.2%; Score 8: DB 4: Langth 244; Best Local Similarity 100.0%; Pred. No. 6.54e-03; Matches 8; Conservative 0; Mismatches 0; Indels 21 SCKASGYT 28 ||||||||| 40 SCKASGYT 47 244 .; 26127 MW; N4CF148B CRC32; 0 Gaps 0

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Query Match 4.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7: DB 4: Length 38: Pred. No. 7.10e-01: 0: Mismatches 0: Indels ő Gaps 0

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1 AVYFCAR 7 ||||||| 111 AVYFCAR 117

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41 PGQGLEW

6

RESULT 36

TD 04321

NC 043221

PRELIMINARY: PRT; 96 AA.

AC 043221

DT 01-30%-1998 (TREMBLEEL 06, CREATED)

DT 01-30%-1998 (TREMBLEEL 05, LAST SEQUENCE UPDATE)

DT 01-30%-1998 (TREMBLEEL 05, LAST SEQUENCE UPDATE)

DE RHEUMATOLD PACTOR RF-ETS (FRANCHIN)

OC EUTHERIA; PRINATES.

DE EUTHERIA; PRINATES.

R1 1010WCE PROW N.A.

R2 1210WCE PROW N.A.

R4 DESCRIPEN WAS NOTIFIED SEQUENCE (1897).

DE EMBL. PROWNER NOTIFIES (266848).

FT NOW\_TER 96

SQ SEQUENCE 96 AA; 1035 MW; 4A5A1C3F CRC32:

Ouery Match 4.6%; Score 7; DB 4; Length 96; Best Local Similarity 104.0%; Peed No. 7:10e-01; Matches 7; Conservative 0; Mismatches 0; Indels 39 PGQGLEW 45 ||||||| 60 PGQGLEW 66 0

RESULT 188

TO 043235

PRELIMINARY, PRT; 100 AA.

AC 042235

PT 01-707-1998 (TREDELERL, 06, CREATED)

DT 01-707-1998 (TREDELERL, 06, LAST ENQUENCE UPDATE)

DT 01-707-1998 (TREDELERL, 06, LAST ENQUENCE UPDATE)

DE RHEUMATOLD PACTON RF-TP16 (PRAGMENT).

OC EUTHERL; PHIATATS.

RE 13/DERREL; PHIATATS.

RE 24/DERREL; PHIATATS.

RE 25/DERREL; PHIATAT

RESOLUTION OF THE PROPERTY OF O43220 PRELIMINARY, PRT: 98 A.
043220 PRELIMINARY, PRT: 98 A.
01-70W-1998 (TREMBLEEL, 06, CREATED)
01-70W-1998 (TREMBLEEL, 06, LAST SEQUENCE UPDATE)
01-70W-1998 (TREMBLEEL, 06, LAST SEQUENCE UPDATE)
01-70W-1998 (TREMBLEEL, 06, LAST SHOTATION UPDATE)
RECHARGOTO PACTOR RF-1P9 (FRAGMENT)
ENDROVA: RECHARGON; CHORDATA; VERTEBRATA; TETRAPODA; MAMALIA;
[] THEREAL: PRAMATES. SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
BOREFIZEN M., NAFIG J.B., THOMPSON K.H.;
MCL. IMMUNOL. 0:0-0(1997).
TREL; AF035784, G2665846: -.
KON TEP

Quary Match 4.8%, Score 7: DB 4; Length 99; Best Local Similarity 10.0%; Bred. No. 7, 10e-01; Matches 7: Conservative 0; Mismatches 0; Indels NON\_TER 98 98 SEQUENCE 98 AA; 10549 MW; A5D79AAD CRC32; 0 Gaps

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Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative Score 7: DB 14: Length 106; Pred. No. 7.10e-01; 0: Mismatches 0: Indels 0

VHA.
HOMO SAPIENS (HUMAN)
EUTARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMALIA;
EUTHERIA; PRIMATES.

ş B Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative 102 DYWGQGT 108 ||||||| 125 DYWGQGT 131 Score 7: DB 4: Length 119; Pred. No. 7:10e-01; 0; Mismatches 0; Indels

RESULT 11

ID 099505 PRELIMINARY: PRT: 122 AA.

AC 099505 PRELIMINARY: PRT: 122 AA.

C 09505 PRT: 197 (PREMELRE, 03, CREATED)

DT 01-MAY-1997 (PREMELRE, 03, LAST SEQUENCE UPDATE)

DT 01-MAY-1997 (PREMELRE, 03, LAST SEQUENCE UPDATE)

DT 01-MAY-1996 (PREMERL, 03, LAST SEQUENCE UPDATE)

DE HEAVY CHAIN PAB FRAGGENT (PRAGMENT)

OS HONO SARIEUS (EMMAN)

OS HONO SARIEUS (EMMAN)

OC EUTHERIA, PRIMATES.

RM (11) PRIMATES.

RM (11) PRIMATES.

US-08-836-455-4.rspt

HORN M.P., VOGEL M., BIAGGI C., MIESCHER S.M., STADLER B.M.;
SUBMITTED (SEP.1996) TO ENBL/GENBANK/DDBJ DATA BANKS.
EMBL; VOB144; E27434;
PPAM; PPO047; 14:
17 1 100M.TER 122 12;
SEQUENCE 122 AA; 13552 MH; CF57BD7D CRC32;

STIRRE

Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative Score 7: DB 4: Length 122: Pred. No. 7.10e-01; 0; Mismatches 0; Indels 0

Gaps

0

110 DYWCQGT 116 |||||||| 125 DYWGQGT 131

EBÖURNCE FROM N.M.
718SUE-BOUR-MARKH:
118SUE-BOUR-MARKH:
118SUE-BOUR-MARKH:
118SUE-BOUR-MARKH:
118SUE-BOUR-MARKH:
118SUE-BOUR-MARKH:
118SUE-BOUR-MARKH:
118SUE-BOUR-MARKH:
118SUE-BOUR-MARKH:
119SUE-BOUR-MARKH:
119SUE-BOUR-M

Query Match

Best Local Similarity 100.0%;
Matches 7; Conservative Score 7: DB 4: Length 129: Pred. No. 7.10e-01; 0: Mismatches 0: Indels Indels 0

Gaps

RESULT 33 ID Q99821 AC Q99821;

PRELIMINARY;

PRT;

136 AA

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RESULT 29
ID 08301 PRELIMINARY: PRT: 106 AA.
AC 083001 PRELIMINARY: PRT: 106 AA.
AC 083001 PRELIMINARY: PRT: 106 AA.
DT 01-NOV-1996 (TREMBUREL 01, CREATED)
DT 01-NOV-1996 (TREMBUREL 01, LAST ANDCENCE OPDATE)
DE E6, E7, E1A, E1B, E3, E4, L1, AND L1 GENES.
GN E4, E7, E1A, E1B, E3, E4, L1, AND L1 GENES.
OS HUMAN PARTICOMNITION TYPE 7.
OC VIRITAR: DS-DIA A.
RI 111 AC SERSENS D. DE STANDARY PROPERTY OF STANDARY PROPERTY PROPERTY OF STANDARY PROPERTY PROPERTY OF STANDARY P

HUMAN PAPILLOMAVIRUS TYPE 7. VIRIDAE: DS-DNA NONEMVELOPED VIRUSES; PAPOVAVIRIDAE; PAPILLOMAVIRUSES

SEQUENCE FROM N.A. DELIUS H., ROY-BURMAN A., GREENSPAN J.S., VOLITER C., HE Y., DELIUS H., ROY-BURMAN A., GREENSPAN J.S., GREENSPAN D., DE VILLIERS E.M.;
GREENSPAN D., DE VILLIERS E.M.;
LINI, J. CANCER 66:453-456(1996),
ENDI. X94164, E72431],
SEQUENCE 106 AA; 11354 MM; F85DB44E CRC32;

₽

22 SCRASGY 28 ||||||| 40 SCRASGY 46

Query Match 4.6%; Best Local Similarity 100.0%; Matches 7; Conservative

Score 7: DB 4: Length 100: Pred. No. 7:10e-01: 0: Mismatches 0: Indels

0

Gaps

Page

8

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Apr 19 13:24:01 1999
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Mon Apr 19 13:24:01 1999

용절당

EMBL: E99494: E350383; -.
HYPOTHETICAL PROTEIN.
SEQUENCE 143 AA; 15771 MW; 48CD792E CRC32;

Gaps

0

US-08-836-455-4.rspt

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Page 42
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RESULT 14

ID 031060

PRELIMINARY: PRI: 143 AA.

AC 031060;
DT 01-JAN-1998 (TREMBLEEL. 05, CREATED)
DT 01-JAN-1998 (TREMBLEEL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLEEL. 05, LAST SEQUENCE UPDATE)
DE RYDOTHETICAL 15.8 AD PROTEIN.

HYDOTHETICAL 15.8 AT PROMITED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

HYDOTHETIC (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

HYDOTHETIC (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

HYD SEQUENCE FROM H. A.

RA PARKHILL J. BARKELL B.G., RAJANDREAM H.A.;

HYD SEQUENCE FROM H. A.

RA PARKHILL J. BARKELL B.G., RAJANDREAM H.A.;

HYD SEQUENCE FROM H. A.

RA BEGUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.6%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 4.6%; Score 7; DB 4; Length 136; Best Local Similarity 100.0%; Pred. No. 7.10e-01; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUP-NOTE MARBOW,
DITTEL, H.J., PARENN P. H.I., BINLEY J.M., SODROSKI J., MOORE J.P.,
BARBAG C.P., BURKON D.R.;
SUBMITTED (DEC-1996) TO EMBLYGENBANK/DDBJ DATA BANKS.
EMBL; USJ267; G.118866;
EMBL; USJ267; G.118866;
EMBL; USJ267; 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER 148
SEQUENCE 148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 13:24:01 1999
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|||||||
125 DYWGQGT 131
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MEDILHE: 9318700.
EIGLMEIER K. BONDRE N., WOODS S.A., CAUDRON B., COLE S.T.;
NOL. MICROBIOL. 7:197-206(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER 136 136
SEQUENCE 136 AA; 14644 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GÖDENCE FROM N.A.
LIAS A.M., MILMER B.C.B.:
DEBL. 1985 (AM-1997) TO EMBL/GENBANK/DDBJ DATA
DBBL. 198523; G118666;
PSPAM; PF00047; 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.
HEDLINE: 91370594.
HERAINA A., MOCENT D.J., MILNER E.C.;
AUTOINGUNITY 8:107-113(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PRAGMENT).
V4-39.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA: PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 PGQGLEW 45
|||||||
60 PGQGLEW 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYCOBACTERIOM LEPRAE.
ROKARYOTA: FIRMICUTES: ACTINOMYCETALES: MYCOBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
ADCOCK K., CHURCHER C.M.;
PEMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 19
20 >148
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15479 MW; B88D2B46 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 7: DB 4: Length 148;
Pred. No. 7.10e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
PLATELET MEMBRANE GLYCOPROTEIN
(GPIB) SPECIFIC ANTIBODY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERTEBRATA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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RE SEQUENCE FOR M. A. RETTIG M.B. HONG C.H., KIM A. LEE J.C.,

RE SEQUENCE 147 AA; 15768 MF; BDDD8F70 CRC32;

SEQUENCE 147 AA; 15768 MF; BDDD8F70 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mon
                                                                                                                                                                                                                                                                                                                                                                                      ID 043305; PRELIMINARY;

AC 01.7001-3999 (TREMELRELL 0.0; LI

AC 01.7001-3999 (TREMELREL  0.0; LI

AC 01.7001-3999 (T
    RESULT 39
ID Q54163
AC Q54163;
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10 099847; PRELIMINAR: PRT: 148 AA.

AC 099847; AC 099847; PREMOLEEL 01, CREATED)

DT 01-MNY-1997 (TREMOLEEL 01, LAST SEQUENCE UPDATE)

DT 01-MNY-1997 (TREMOLEEL 04, LAST SEQUENCE UPDATE)

DT 01-WNY-1998 (TREMOLEEL 05, LAST ANNOTHING UPDATE)

DT 01-WNY-1998 (TREMOLEEL 05, LAST ANNOTHING UPDATE)

DT 01-WNY-1998 (TREMOLEEL 05, LAST ANNOTHING UPDATE)
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                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                          PRODUCENCE FROM N.A.

PRODUCENCE FROM N.A.

WILSON R. AINSCOUGH R., ANDERSON K., BANNES C., BERKS M., BONFIELD J.,

WILSON R., AINSCOUGH R., COPERT T., COOPER J., COULSON K., CRANTON M.,

M. DENKYN J., CONNELL M., COPERT T., COOPER J., COULSON K., CRANTON M.,

WILSON R., DO S., DORBER R., ANTERLIA D., ORNESTON L., CARRINER M., CREEN P.,

WARKINS T., HILLER W., JUTEM M., DORRSON J., LOOPE C.,

WARKINS J., LAISTER M., ANTERLIAD P., LOGHNING J., LLOID C.,

WARKINS J., LAISTER M., ANTERLIAD D., SHONNEER R., SANLOON M., SHITH A.,

WARKINS J., WORLINGS B., O'CALAGIAN M., PARSONS J., PERCY C.,

WARKINS J., WORLINGS B., O'CALAGIAN M., PARSONS J., PRICH A.,

WALKINSON STROAT J., WHILDRAN J., PRICHEST H.E. J., TROMAS K.,

WALKINSON STROAT J., WHILDRAN P.,

WALKINSON STROAT J., WHILDRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apr 19 13:24:01
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 4.6%;
Best Local Similarity 100.0%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECURNCE FROM N.A.
MEDILNE, 6607149.
CAO J. VESCIO R.A., RETTIG M.B., HONG C.H., KIM A., LEE J.C.,
LICHTENSTII A. A.K., BEREESSON J.R.;
LETUENIA 9:1948-1951(1995).
EMBL: $80860: 5244688: -
FPAM: PROGO47; 19.
NOM_TER
147 AA: 15768 MW; BDDDD8F70 CRC32;
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|||||||
88 SLTADTS 94
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125 DYWGQGT 131
                                                                                                                                                     53 PLPLLSI
|||||||
7 PLPLLSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEOURNCE FROM N.A.
JUDNITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 QSGAELV 102
|||||||
25 QSGAELV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enorhabditis elegans.
Raryota; metaloa; acoelomates; mematoda; secernentea; rhabditida
                                PRELIMINARY;
                                                                                                                                                          59
13
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 7; DB 4; Length 198; Pred. No. 7:10e-01; O; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7: DB 4: Length 147:
Pred. No. 7.10e-01:
0: Mismatches 0: Indels
                                                                                                                                                                                                                                                                     Score 7: DB 5; Length 251; Pred. No. 7.10e-01; O; Mismatches O; Indels
                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                299 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-836-455-4.rspt
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Gaps

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Page 44

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Mon
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O457
O10-1-7
O1
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AC 046
AC 01
AC 01
AC 04
AC 02
AC 04

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                              Query Match 4.8; Score 7. DB 5: Length 998; Best Local Similarity 100.0; Peed No. 7.DB 6: Length 998; Matches 7: Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%; Pred. No. 7.10e-01:
Matches 7: Conservative 0; Mismatches 0: Indels
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                                                                                                                                                                                                                                                                                                                          RECUENCE FROM N. ANDERSON K. BAYMES C., BERKS H., BONFIELD J., BURRON R. ANDERSON R. ANDERSON R. CRAXTON M., CRAXT
                                                                                                                                                                                                     SEQUENCE 998 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PREBILI, BARNES G.T., CHEN J., CHURCH D., BUCKLER A., BAXENDALE S.,
BATES G. P. LEHRACH H., GUSELLA H.J., DUTAO H.P., AMBROSE C.M.,
MCDONALD H.E., GUSELLA J.F.;
SUBMITTED (JAN-198) TO EMELJAGENBANK/DDBJ DATA BANKS.
EMBL. ATO409464 C.3792154; -
HTPOTIETICAL PROTEIN.
NOW_TER
1. SEQUENCE 604 AA: 69751 MW: 5P5D1CDA CRC12;
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EMBL: L14842: G294897;
SEQUENCE 299 AA; 32565 MW; 95651FDD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 ISSLTSE 321
|||||||
102 ISSLTSE 108
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MEDLINE: 56171776.
RICHARDSON P.T., PARK S.F.;
MICROBIOLOGY 141:3191-3191(1995).
EMEL. X88649; E199811.
SEQUENCE 322 AA; 35557 MW; 386569FB
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STRAIN=YSH6200;
MEDLINE: 94328936.
HOBBS M., REEVES P.I
MOL. MICROBIOL. 12:6
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Q46003; PREMBLREL:
)1-NOV-1996 (TREMBLREL:
)1-NOV-1996 (TREMBLREL:
)1-NOV-1996 (TREMBLREL:
TG START
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BESHAW J.;
EMMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43
5724 PRELIMINARY: PRT: 998 AA.
15724 PREMBLREL O6, CREATED)
1-JUN-1998 (TREMBLREL O6, LAST SEQUENCE UPDATE)
1-JUN-1998 (TREMBLREL O7, LAST SEQUENCE UPDATE)
1-AUC-1998 (TREMBLREL O7, LAST ANNOTATION UPDATE)
1-AUC-1998 (TREMBLREL O7, LAST ANNOTATION UPDATE)
1010.13 (FRAGENT).
ARNOTHABDITIS ELECANS.
ARNOTHABDITIS ELECANS.
ACOCKLONATES; NEMATODA; SECERNEWIEA; RHABDITIDA.
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STRAIM-TSH5200;
MEDLINE: 94299218.
MAJAKUMAR K., JUST B.H., SASAKAWA C., OKADA N., YOSHIKAWA
ADLER B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHIGELLA FLEXMERI.
PROKARTOTA: GRACILICUTES; SCOTOBACTERIÀ; PACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
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01-NOV-1996 (TREMBLREL. 01,
01-NOV-1996 (TREMBLREL. 01,
DTDP-6-DEOXY-D-GLUCOSE-3,5 RFBC.
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ROKARYOTA: GRACILICUTES: SCOTOBACTERIA;
ROKARYOTA: GRACILICUTES: AND/OR VIBRIOID.
                                                                                                                                                                                                                                                                        2 368:32-38(1994).
292811; E1247172; -
                                                                                                                                                                                        110111 MW; 8478DC1B CRC32;
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:855-856(1994).
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1, LAST SEQUENCE UPDATE)
11, LAST ANNOTATION UPDATE)
5 EPIMERASE.
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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PRESULT 45
ID 05525 PRELIMINARY;
AC 05525, OF 01-001-198 (TREMBLREL. 0
DT 01-001-1998 (TREMBLREL. 0
DT 01-MG-1998 (TREMBLREL. 0
DE 070CLIN.
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AC 063799;
AC 063799;
DT 01-MG-1998 (TREMELEL, 0
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ID 044505;
AC 044505;
DT 01-70N-1998 (TREMBLREL, 05, CREATED)
DT 01-70N-1998 (TREMBLREL, 06, LACT SEQUENCE UPDATE)
DT 01-70N-1998 (TREMBLREL, 07, LACT SEQUENCE UPDATE)
DT 01-70N-1998 (TREMBLREL, 07, LACT SEQUENCE UPDATE)
DE HYDOTHETICAL 69.8 KD PROTEIN (FRANCHENT).
OS HOMO SADEINS (HOMAN)
OS EUTHREN, PRINATES.
DE SEQUENCE PROM N.A.
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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|||||||
63 GLEWIGN 69
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MEDLINE; 88089537:
HUGHES P.J., NORTH,
J. GEN. VIROL. 69:4:
EMBL; D00239; D1000;
POLYPROTEIN; PROTEAL
CHAIN
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Best Local Similarity 100.0%;
Matches 7; Conservative
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|||||||
101 QISSLTS
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SEQUENCE 399 AA; 43151 MW;
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|||||||
75 GDTYYNQ 81
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STALMHSCHELOSE

KULAKOV L.A., LARKIN H.J.:

SUBHLITTED (LPR-1998) TO EMEL/GENEANK/DDBJ DATA

EMEL. AJOSSES; E1288484; ...
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EUBACTERIA: FIRMICUTES; ACTINONYCETES; NOCARDIOFORM ACTINONYCETES;
RISDCCOCCUS.
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|||||||
11 LSITTGV 17
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8105 PRELIMINARY. PRI 2157 AA.
8105 PRICE PRI 2157 AA.
1-NOV-1996 (PREMELREL OJ CASENTE).
1-NOV-1996 (PREMELREL OJ CAST SEQUENCE DOATE)
1-NOG-1998 (PREMELREL OJ LAST ANNOTATION UDDATE)
1-NOG-1998 (PREMELREL OJ LAST ANNOTATION UDDATE)
1047807ERIM PRECURSOR.
1048 RAINOVIGUES 18 (REV-18).
                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NORTH C.
E. 69:49-
D100061
PROTEASE
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-58(1988)
                        06, CREATED)
06, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (; PRT; 2157 AA. (92109; Q82112; Q82109; Q82110; Q82111; Q82112; Q., CREATED)

O7, LAST SEQUENCE UPDATE)

O7, LAST ANNOTATION UPDATE)
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V92 PROTEIN
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V97 PROTEIN
V97 PROTEIN
V97 PROTEIN
V98 PROTEIN
V99 PR
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Pred. No. 7.10e-01;
0; Mismatches 0; Indels
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Pred. No. 7.10e-01;
0; Mismatches 0; Indels
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                        PRT; 2910 AA.
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Pred. No. 7.10e-01;
0; Mismatches 0; Indels
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Mon Apr 19 13:24:01 1999

US-08-836-455-4.rspt

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RESULT 50

DD 041403;

AC 041403;

AC 041403;

DT 01-807-1996 (TREMELEEL 01 CREATED)

DT 01-807-1996 (TREMELEEL 01 LAST SECRETE PARTE)

DT 01-807-1996 (TREMELEEL 01 LAST SECRETE)

DT 01-807-1996 (TREMELEEL 01 LAST SECRETE)

DE EARLY MODULIN (SMODI-3N) PROTEIN (FRAGMENT).

OC EUKARTOTA: PLANTA: DEBRYOPHTYN; ANGIOSPERMAE; DICOTTLEDONEAE; FABALES;

RN [1]

RR SEQUENCE FROM N.A.

STRITMATTER 6., CHIA T.F., TRINH T.H., KATAGIRI F., KUHLEMEIER C.,

RA CHIA M.H.;

HOLD PLANT HORDEE INTERACT. 0:0-0(0).

DR MODI, FLANT HORDEE INTERACT. 0:0-0(0).
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IN THE PROPERTY AND ACTION OF THE PROPERTY AND ACTION.

AC 197465; PRECIMINARY; PRT; 12 AA.

AC 297465; PRECIMINARY; PRT; 12 AA.

AC 297465; PRECIMINARY; PRT; 12 AA.

DE 701.MX-1997 (TRECIMINE) OJ. LAGT SECOURNE UPDATE)

DE 800.MARCOTA, MATHAMIES, CHORDATA; VERTZERATA; TETRAPODA; MAMMALIA;

RE 11

RE 500.MARCOTA, MATHAMIES, CHORDATA; VERTZERATA; TETRAPODA; MAMMALIA;

RE 500.MARCOTA, MATHAMIES, CHORDATA; TETRAPODA; MATHAMIES, CHORDATA;

RE 500.MARCOTA, MATHAMIES, CHORDATA; TETRAPODA; MATHAMIES, CHORDATA;

RE 500.MARCOTA, MATHAMIES, CHORDATA; TETRAPODA;

RE 500.MARCOTA, MATHAMIES, CHORDATA; TE
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Best Local Similarity 100.0%;
Matches 6; Conservative
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Best Local Similarity 100.0%;
Matches 6; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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126 YWGQGT 131
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147 PLVPGSL 153
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01-71N-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-71N-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-71N-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
CYSTELER PROTENSE (FRAGMENT).
ENTANOERA DISPAR.
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STRAINBEALDG:
MEDILHE: 98070772.
COMEN-SALVON N. EL-AMENOUI A., LEHBOVICI N., PETIT C.;
PROC. NATL. ACAD. SCI. U.S.A. 94.14450-14455(1997).
SEQUENCE 2910 AA: 313410 NM; 94F5C68E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER 56 56 56
SEQUENCE 56 AA; 6541 MW; D226FC87 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 105-116 FROM N.A.
HEDILINE: 86043880.
CLEARY M.L., SKLAR J.
PROC. NATL. ACAD. SCI. U.S.A. 82:7439-7443(1985).
EMBL. N11931, 20139489 .
SEQUENCE 12 AA: 1297 NM; 1993EA44 CRC32;
CHUA N.H.;
CHUA N.H.;
MOL. PLANT MICROBE INTERACT. 0:0-0(0).
EMBL; M23314; G169878; -.
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EUKARVOTA: METAZOA, CHORDATA; VERTEBRATA: TETRAPODA: MAMBALIA:
EUTHERIA: RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 NQKFKG 26
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80 NQKFKG 85
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TRAINEAGM 142:
MATTACHARTA A., SHARMA R., AZAM A., BHATTACHARTA S.;
UBHITTED (AUG.1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
MBL, ARO19736, G2444279;
ROTEASE.
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7 FLFLLS 12
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Pred. No. 7.10e-01;
0; Mismatches 0; Indels 0; Gaps
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Pred. No. 4.74e+01;
0; Mismatches 0; Indels 0;
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Pred. No. 4.74e+01;
0; Mismatches 0: Indels
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Page 52

Search completed: Thu Apr 15 18:10:46 1999 Job time: 77 secs.

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RESULT 48

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Db 3 PPPVYP 8
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BAY. J. Immunol. (1993) 23:3503-2510

Pariable region gene selection of immunoglobulin G-expressing

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Seat Local Similarity 100.0%; Pred No. 4.94e-28;
Matches 20; Conservative 0; Minatches 0; Indels 0;
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps
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19 heavy chain precuracy V region (4C11) - mouse (fragment)

20 heavy chain precuracy V region (4C11) - mouse couse

20-bun-1982 Sesquence_revision 10-Jun-1992 Stext_change

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antificityphy monoclonal authory from the MEZ
Leminised with antiarenate antibodies (Also from A/J
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ACCESSIONS REFERENCE Pauthors

RESULT ENTRY TITLE ORGANISM DATE

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•		523 29 NO8	W XXGAADISO	Mouse immunoglobulin h	6.65e-10		•	synthetic construct.	
	962 31 6.7	520 29 XOS			6.650-10		ORGANISM A	artificial sequence.	
	31 6.7	8	MOSICHVEC H	House Ig germline H-ch	6.65e-10			1 (bases 1 to 902)	
	31 6.7	593 29 MO8	_		6.65e-10		RS	hen, E.C., Cockburn, W., Torrance	Chen, E.C., Cookburn, W., Torrance, L., Barker, H. and Whitelan, G.C.
	31 6.7	29		House embryo Dan for 1	6.65e-10		TITLE	Acobramic woommiration of w so	Cytopinamic modumutation of a soluble indecisoral solv process to a
	31 6.7	29	2	Mouse Ig active H-chai	6.656+10			THE ATTENDED TO THE PARTY OF TH	Prent Print expressed as a chromodyni theory in detretions over
	6.7	29		Differentiated mouse 9	5.55e-10		REFERENCE 1	2 (bases 1 to 902)	
	31 6.7	815 29 YOU	MOTGVH12 X	Mouse immunoglobulin J	6.656-10			hen.E.C., Cockburn,W., Torrance	Chen, E.C., Cockburn, W., Torrance, L., Barker, H. and Whitelam, G.C.
	31 6.7	2		tue musculus mana for	6.65e-10			Direct Submission	
	31 6.7	29	_	lus musculus clone B2c	6.65e-10		F	Submitted (23-FEB-1996) E C. Chen, Botany, Univ. of Leicester,	in, Botany, Univ. of Leicester,
	31 6.7	29	_	dus musculus (B5e) hea	6.65e-10			University Road, Leicester LEI /KH, UK	ZRH, UK
	31 6.7	29	_	tus musculus (C25c) he	6.65e-10		FEATURES	Tocation/Anatities	
	31 6.7	2		tus musculus (Blae) ne	0.000110		-0410	/organisme"synthetic co	matruct.
	31 6.7	961 29 MOS	MOSBON H	Kus musculus (BSc) hea	6.656-10			/note="PCR synthesized	/note="PCR synthesized gene from mouse hybridoma cell line
	31 . 6.7	29		Nue musculus clone C9g	6.65e-10			SCR 40°	
	31 6.7	29	ž	M.musculus mRNA for mo	6.65e-10		}	/db_xre: "taxon: 32630"	
	31 6.7	32		ynthetic construct RF	6.65e-10		CDS.	At 000	
		: 2	-	MOUSE 19 9 THAT SELECT				/transl table=11	
	30 G.S.	307 29 MI		Nouse hybridoma 8335 m	5.11e-09			/product="single chain Fv antibody"	Fv antibody"
	30 6.5	29	1007070016 м	Mus musculus Ig heavy	5.11e-09			/db_xref="PID:g1236091"	
	30	2		Mouse hybridoma germ 1	5.11e-09			ASSERTATION TO A SECTION OF THE SECT	CCESPOILVESARTIA ECVOSRESGEGEGEGEGESEKINSIOPEDEGESTCOHETOTEST / CIRCULTATION - SAFEAND VILLULAROSSON SELVILLICANS SAFESARTOTEST
				THE RESCRIPT PRINCES	K 11000			PGGGTELEIRRADAAPTVSIFPP	PGGGTELEIRRADAAPTVSIFPPSSPGGGGGGGGGGGGGGGGGGVDQVQQPGAELVRSGA
	o. o	354 29 308	MUSICIAN H	H-Mus musculus IdM ant	S. 116:09			SVEMSCKASCTTPTSYNGHVKQ	Svensckasgytpysyndhavkojpgoglemigyiypghggyiynokpkgkatltadt
	30 6.5	5		cDMA encoding fragment	5.110-09			SSSTANOQISSLTSEDSAVYFCA	SSSTANDIGISSLISEDSAVTFCARGDIRNDFFDFWGQGTTLTVSSAKTIPPSVTFLAP
	30 6.5	29	ş	Mus musculus Ig active	5.11e-09			TEGNOSCOPETAPEDPED.	
	30	2		M.musculus mRNA for im	5.110-09		DAME COUNT	223 8 223 9 224	200 €
		3 6	TIJORO A	Rouse 19 gamma chain m	W. 119-00		971917		
	30 6.5	29	6	Mouse Ig mu-chain (358	5.11e-09	-	Query Match	21.0%;	Score 97; DS 32; Length 902;
	30 6.5	29	=	House Ig rearranged ga	5.11e-09		£	Similarity 99.2%; Pred. No. 2	Pred. No. 2.89e-78;
		2		cDMA encoding single c	5.110-09		MATCHES 1		comes t) todate of cabe of
	30 6.5	29	6	Nus musculus recombina	5.11e-09				CANCARCE CONTROL AND CONTROL ST.
	30	25 Z9 X0S			9.110:00 9.110:00		111		
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Dest Local Similarity 98.6%; Pred. No. 9.39=61;
Matches 141; Conservative 0; Misnatches 2; Indels 0; Gaps 0;
116 CTGGGGCTTAGTAMAINTICTGCAGGCCTTGGGCTACAGTTTAGGGTTACATTA 159

98 CTGGGGCTTAGTAGTAGTAGTAGTAGTGTGTGTGTGCAGTTAGAGTTACATTACAGTTACATTACAGTTACATTACAGTTACATTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACATTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGTTACAGT
                                                                                                                                                                                                                                         Paradian, V-region; immunoglobulin heavy chain; processed gene. Was masculus cDMA to BMMA.

Mas masculus blanchine the processed gene. Was masculus blanchine the processed gene. Was masculus blanchine the processed general section of the processed general section of the processed general to 458).

In Chases 1 to 458).

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In Chases 2 to 458 p. Nurray, E.D.Jr., Ledbetter, J.A., Malitroom, J. and Heilbetter, K. E., Warray, E.D.Jr., Ledbetter, C.A., Malitroom, J. and Heilbetter, Marian bloody to corol of the processed general bloody to activity of the processed general proc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B805045 PROFILE AND COMPUTER-readable sequence [1] kindly submitted by A.T.Liu, 02-FEB-1987.
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105921 458 bp
DEFINITION Sequence 37 from Patent EP 0274394.
ACCESSION 105921
NID 9590876
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Best Local Similarity 98.6%; Pred. No. 9.39e-61;
Matches 141; Conservative 0; Missatches 2; Indels 0; Gaps
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AUTHORS

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RETWORDS SOURCE ORGANISM LOCUS DEFINITION ACCESSION WID

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572 GGATTGGA 579
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197 GGATTGGA 204
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77 CTREGOCTUAGTOSTRAGOTETOGOCCTEAGTAMAATCTCCTCCAAGGCTTCTGGCT 116
78 CTREGOCCTUAGTOSTRAGOTETOGOCCTEAGTAMAATCTCCTCCAAGGCTTCTGGCT 116
                                                                                                                                                                                                                                                                                                                                                                                                             ITCRASEHIYSYLAWYQOK
OPEDFGSYYCQHHYDTPRI
GGSYDQVQQPGAELVRSGA
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RESULT 1 LOCUS DEPIMITION

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969 29 MUSEGE

Mus musculus (C6e) hem 5.11e-09

ACCESSION NID RETWORDS

zgrassiz 902 bp m884, Synthetic single chair by antibody against potato virus V coat protein, m884, partial cds. 04992 91336990

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Robinson, R. F., Liu, A. T., Hellstrom, K. E., Hellstrom, I. and Robinson, R. E., Liu, A. T., Liu
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RETWORDS house mouse.

SOURCE Nus musculus

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House Ig kappa 1

H220-23

H320-23

H320-31

V-region: immun
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Correlation between sometically derived VH-CDR1 (
Perilation for DNA among autoimmune antibodies (
J. LERNING). (1997) In press
J. Chases 1 to 102)

Although T. N. (1997) In press
Light Statistion
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Vertebrata; Eutheria; Rodentia; Bciurognathi;
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Sited (18-APR-1986) Tony N. Marion, Dept. of
Sited (18-APR-1986) Tony N. Marion, Dept. of
subblogy/Immunology, University of Tennesse, 858 Madison
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Best Local Similarity 98.6%;
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**Alseo

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"Naler,", Caton, N. J., Staudt, L. M., Schwarts, D. and Gerhard, W.
waler, J., Caton, N. J., Staudt, L. M., Schwarts, D. and Gerhard, W.
set of closely related antibodies dominates the primary antibody
sponse to the antigenic site CB of the A/PK/8/34 influenza wirus
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(strain BAIB/c), cDNA to mRNA,
usculus
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RAULE, N.

rect Submission

baitted (24-VUL-1997) Immunology,

Rochater, MD 55905, USA

Location/Qualifiers
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/ub_species="domestious"
/ub_tref="taxon:10090"
/csll_line="H230-23"
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0; Mismatches 3; Indels 0;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Apr 15 18:00:56 1999; MasPar time 8.71 Seconds 657.976 Million cell updates/sec

**Sular** output not generated.

Description: Perfect Score: Sequence: Title: >US-08-836-455-4 (1-153) from US08836455.pep 1109

1 MECSWVFLFLLSITTGVHSQ.....TVSSAKTTPPPVYPLVPGSL 153

Scoring table: PAM 150 Gap 11

Searched: 116695 seqs, 37453910 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir58 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 42.120; Variance 104.479; scale 0.403

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

1t	Score	Query Match	Length	8	Ib	Description	Pred. No.
	783		475	ນ	S01321	Ig gamma-2b chain pre	4
N	780	70.3	474	N	S25057	gamma-2b chain	1.38e-10
w	774		469	N	S37483	gamma-2a	e-1
4	767		151	N	PL0011	Ig heavy chain precur	2.00e-10
ر.	763	•	150	N	PN0444	heavy chain	9.21e-10
6	746	•	139	N	PS0024	heavy chain pr	ņ
7	742		166	N	PL0012	heavy chain	Ņ
<b>&amp;</b>	727	٠	137	N	H32513	heavy chain	8.5
9	724		246	N	S38950	gamma chain	N
10	724	٠	446	N	S40295	gamma-2a chai	2.6
11	710	٠	178	N	S29594		•
12	709		140	_	HVMSG7	Ig heavy chain precur	8.1
13	708		138	N	S21810	heavy chain V	1.19e-
14	705	•	140	N	PH1482	heavy chain v	3.74e-
15	697	•	140	N	PH1489	Ig heavy chain V regi	7.84e-9
16	692		138	N	E32513	heavy chain pr	5.25e-9
17	686		140	N	PH1488	heavy chain	5.13e-
18	685	•	136	N	PL0208	heavy chain pr	7.50e-
19	684	•	141	N	A39276	Ig heavy chain precur	٠,
20	681	61.4	140	N	PH1484	heavy chain	3.43e-
21	678	61.1	139	N	A27609	heavy chain pr	1.07e-
22	676	61.0	135	N	A30577	heavy chain	2.29e-
23	675	60.9	135	N	PS0057	heavy chain	w

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## ALIGNMENTS

120	Db 61 GQGLEW	Db 1 MEWIWI   1:	Query Match Best Local Similarity Matches 110; Conse	1-19 20-475 159-223 SUMMARY	CLASSIFICATION KEYWORDS	#accession ##molecule ##residues ##cross-re ##note	#cross-refere	#journal	ACCESSIONS REFERENCE #authors	RESULT 1 ENTRY TITLE ORGANISM DATE
120 QVGLLPFGYMGQGTLYTASAAKTTPPSVYPLAPG 153 	GQGLEWIGETYPGSGNSYFNEKFKGKATLTVDKSSSTAYLHLSSLTSEDSAVYFCA-GPR 119          ::  :  :  :	MEMIWIFLFILSGTAGVOSQVOLQQSGAELARPGASVKLSCKASGYTLTSYGISWVKQRT 60     :  :    :	h 70.6%; Score 783; DB 2; Length 475; Similarity 71.4%; Pred. No. 4.38e-106; 110; Conservative 22; Mismatches 18; Indels 4; Gaps 3;	#domain signal sequence #status predicted #label SIG\ #product Ig gamma-2b chain #status predicted #label MAT\ #domain immunoglobulin homology #label IGGI #length 475 #molecular-weight 51567 #checksum 4120	gene #superfamily immunoglobulin C region; immunoglobulin homology immunoglobulin	cession \$0131 ##molecule_type mRNA ##residues 1-475 ##label DE1 ##coss-references EMBL:X13188; NID:g51780; PID:g51781 ##prote this sequence was determined from the differentiated	immunoglobulin directed against the tumour marker human placental alkaline phosphatase. #cross-references MUID:88329081	Fiers, W. Eur. J. Biochem. (1988) 176:287-295 Eur. J. Biochem. (1988) 176:287-295	S01321 S01320 de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.;	\$01321  #type complete Ig gamma-2b chain precursor - mouse #formal_name Mus musculus #common_name house mouse 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 08-Sep-1997

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                                         AGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCCTACAAT
                                                                                                             TGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAGCAGACACCT
                                                                                                                                                  ATGGGATICAGCAGGATCTTTCTCTTCTCCTGTCAGTAACTACAGGTGTCCACTCCCAG
                                                                                               TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCT
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Production of a mouse-human chimeric monoclonal antibody to CD20
with potent Fc-dependent biologic activity
J. Immunol. 139, 3521-3526 (1987)
                                                                                                                                                                                                                                                                                    Similarity
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Liu.A.Y., Robinson, R.R., Murray, E.D. Jr. ., Ledbetter, J.A.,
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lu, 02-FEB-1987.
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/codon_start=1
/product="immunoglobulin heavy chain"
/product="finunoglobulin heavy chain"
/db_xref="pID:g196224"
/translation="MGFSRIFLFLLSVTTGVHSQAYLQQSGAELVRPGASVKMSCKAS
GYTTTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSSTAYMQL
SSLTSSDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVS"
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/organism="Mus musculus"
121 c 111 g 113 t.
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                                       Robinson, R.R., Liu, A.Y., Hellstrom, K.E., Ledbetter, J.A.
Patent: WO 8804936-A 12 14-JUL-1988;
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105921
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

lar output not generated. Thu Apr 15 17:57:49 1999; MasPar time 8.66 Seconds 627.099 Million cell updates/sec

Description: Perfect Score: Sequence: Title: ..>US:.08-836-455-2
(1-145) from US08836455.pep
1019
1 MGAPAQILGELLLLEPGTRC.....IKRADAAPTVSIFPPSSKLG 145

Scoring table: PAM 150 Gap 11

Searched: 116695 seqs, 37453910 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

pir58 1:pir1 2:pir2 3:pir3 4:pir4

Database:

Statistics: Mean 42.409; Variance 104.536; scale 0.406

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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e protein	##molecule_ty
A94239	*accession A9
MUID: 67056897	#cross-references MUID:67056897
hanism of antibody synthesis: size differences between	
Science (1967) 155:465-467	
y, W.R.; Dreyer, W.J.; Hood, L.	TS.
A94239	RESERENCE A9
met-3 is apparently used as an afternative initiator in 25% of the chains	***************************************
	##residues
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A93815	#accession A9
MOID: 77148916	*cross-reference
kappa-type light chains.	•
f the precursors of mouse immunoglobulin lambda-1-type and	
lino acid sequence of the NH-2-terminal extra piece segments	#title Am
Proc. Natl. Acad. Sci. U.S.A. (1977) 74:716-720	# Journal Pr
Burstein, Y.; Schechter, I.	
A93815	
gene MOPC 41 and the germline gene VK41	
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17 ##label VK41	##residues
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893211	#accession B9
1-130 ##label PC41	**residues
e DNA	##molecule_type DNA
A93211	#accession A9
MUID:79221900	*cross-references MUID:79221900
recombination without further somatic mutation.	
appa-immunoglobulin gene is formed by site-specific	
ure (1979) 280:370-375	
dman, J.G.; Max, E.E.; Leder, P.	#authors Se
A93211	REFERENCE A9
A93211; B93211; A93815; A94239; A01922; A01923	ACCESSIONS A9
16-Aug-1996	
24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change	
*formal name Mus musculus *common name house mouse	
chain precursor V region VK41	SNI
pa ch	
KVMSM4 #type complete	
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Anti-DNA antibodies from autoimmune mice arise expansion and somatic mutation.
                                                                                                                               #length
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Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
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16-Sep-1992 *sequence_revision 16-Sep-1992 *text_change
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                                                                                                                               #region
gth 106
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#region framework 2\
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*region framework 3\
*region complementarity-determining
*region framework 4
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#domain immunoglobulin homology #label IMM\
#disulfide_bonds #status predicted
#th 130 #molecular-weight 14311 #checksum 6707
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92.2%;
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                                                                   Pred.
                                                                               Score 690; DB 2;
Pred. No. 4.05e-91;
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                                                                  Mismatches
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                                                                                                       **CITLE EUR. J. BLOCHEM. (1990) 192:767-775
CONSTRUCTION and Characterization of a monoclonal antibody directed against harmonics MUID:91006173
***Cross-references MUID:91006173
***accession S14237
***molecule ******
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors
                                                                                             *#molecule_type mRNA
*#molecule_type mRNA
*#residues 1-234 ##label VAN
                                                                                ##cross-references EMBL:X56394; NID:g51622; PID:g51623
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Similarity 69.0%;
98; Conservative
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Similarity 92.5%;
98; Conservative
                                                       heterotetramer; #length 234 #mc
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Ig kappa chain precursor (15C5) - mouse
#formal_name Mus musculus *common_name house mouse
25-Feb-1994 *sequence_revision 10-Nov-1995 *text_ci
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Anti-DNA antibodies from autoimmune mic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PL0259 #type fragment
Ig kappa chain V region (anti-DNA, DP11VK) - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
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#molecular-weight 26087
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  Score 686; DB 2;
Pred. No. 1.87e-90;
16; Mismatches 28
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Pred. No. 8.69e-91;
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Best Local Similarity 94.8%;
Matches 361; Conservative
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GGGACCAAGCTGGAAATAAAA 381
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           Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 381)

O'Connor, K.C., Farrell, T.P., Morikawa. A. and Stollar, B.D. anti-DNA antibodies of normal mice immunized with poly(dC) are structurally similar to natural autoantibodies
                                                                                                                                                                                          AF045510 381 bp mRNA ROD 28-FEB-1998
Mus musculus 6C9 monoclonal antibody kappa light chain variable
region, (IgK) mRNA, partial cds.
AF045510
                                                                                                                      Mus musculus
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61. .345
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346. .>381
/gene="IgK"
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/translation="MRAPAQIEGETLLLEPGTRCDIQMTQSPSSLSASLGERVSLTCR
ASQDIGNSLNWLQQEPDGTIKRLIYATSSLDSGVPKRFSGSRSGSDYSLTISSLESED
FVDYYCLQYASFPWTFGGGTKLEIK"
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/product="ant1-poly(dC) monoclonal antibody kappa light
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/cell_line="spleen cell hybridoma"
/chromosome="6"
/clone="dC4"
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1. .>381
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O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B
Direct Submission
gamma-immunoglobulin; I(
    region; variable region
    house mouse.
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                                                       M.musculus mRNA for X02177
                                                                                   MMIGGVJ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.5%;
Similarity 94.2%;
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/strain="057BL/6"
/db_xref-"taxon:10090"
/cell_line-"spleen cell h
/chromosome-"6"
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346. .>381
/gene="IgK"
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61. .345
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/db_xref-"PID:92906104"
/translation-"MRAPAQIFGFLLLLFPGTRCDIOMTQSDSSLSASLGERVSLTCR
ASQDIGSSLSWLQQEPDGTIKHLIYATSSLDSGVPKRFSGSRSGSDYSLTISSLESED
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Pred. No. 9.33e-264;
0; Mismatches 22;
                          Ig light chain;
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                                                                   RNA RC kappa light chain
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M.musculus
X02178
g51899
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l Similarity 92.1%;
350; Conservative
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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Darsley,M.J. and Rees,A.R.

Nucleotide sequences of five anti-lysozyme monoclonal antibodies

EMBO J. 4 (2), 393-398 (1985)
                                            MMIGGVJ2
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326. .364
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/db_xref="pID:g063215"
/translation="FGFLLMEPGTRCDIQMTQSPSSLSASLGERVSLTCRASQEISG
/translation="FGFLLMEPGTRCDIQMTQSPSSLSASLGERVSLTCRASQEISG
YLSWLQQKPDGTIKRLIYAASTLDSGVPKRFSGSRSGSDYSLTISSLESEDFADYYCL
QYLSVPLTFGAGTKLELKRADAAP"
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365. .>380
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306. .3
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93 c 89 g 110 t
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/db_xref="taxon:10090"
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kappa light chain (p
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l Similarity 91.3%;
347; Conservative
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region; variable region
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Darsley,M.J. and Rees,A.R.
Nucleotide sequences of five anti-lysozyme monoclonal antibodies
EMBO J. 4 (2), 393-398 (1985)
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MUSIGKCMA
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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/db_xref="piD:g663216"
/translation="VFGFLLLWFPGTRCDIQMTQSPSSLSASIGERVSLTCRASQEIS
GYLSWLQQKPDGTIKRLIYAASTLDSGVPKRFSGRRSGSDYSLTISSLESEDFADYYC
LQYLSYPLTFGAGTKLELKRADAAP"
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366. .>381
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/db_xref="taxon:10090"
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Pred. No. 2.35e-243;
0; Mismatches 33;
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\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* (MT)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

erch\_pp 9 :: protein - protein database search, using Smith-Waterman algorithm Tue Mar 23 15:01:25 1999; MasPar time 2.89 Seconds 61.491 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-766-350A-2 (24-34) from US08766350A.pep (2 of 4) 63 1 MTQSPSSLSAS 11

Sequence:

Scoring table: PAM 150 Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 15:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part12 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 15.144; Variance 52.220; scale 0.290

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Result No.
<b>3</b>	Score
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104 105 105 105 105 105 106 106 106 107 107 107 107	Length
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Query Match 100.0%; Best Local Similarity 100.0%; Matches 11; Conservative

Score 63; DB 29; Le Pred. No. 3.52e+00; 0; Mismatches 0;

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## ALIGNMENTS

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(HDN) in subsequent pregnancies. In addition, anti-Rhesus D (HDN) in subsequent pregnancies. In addition, anti-Rhesus positive blood immunoglobulin can be used after mistransfusions of Rhesus positive blood to Rhesus negative recipients in order to prevent sensitisation to the to Rhesus D antigen. The products can also be used as diagnostic reagents. Sequence 104 AA;		Y 1 W52225 standard; Protein; 104 AA. W52225 standard; Protein; 104 AA.

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RESULT

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                                                                                                                                                                                                                                                                                                                                                                                  region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric Mus musculus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised alpha-4 integrin antibody 21.6 VL La. Alpha-4 integrin; humanised antibody; monoclona
                                                                                                                                                                                          misc_difference
                                                                                                                                                                                                                                                                                                    misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W22412 standard; Protein;
                      region
                                                                                                       region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Rhesus D antigen binding
Rhesus D antigen in therapy,
thrombocytopenic purpura
Claim 1; Fig 5B; 68pp; Englis
This sequence is the antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; V19745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vogel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 100.0%;
Local Similarity 100.0%;
hes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-1997;
24-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 mtqspsslsas 12
|||||||||||
| 24 MTQSPSSLSAS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98-077173/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP-810421
                                                                                                                                                                                                              21.6 VL, in CDR2 loop"
                                                                                                                                                                                                                                                                                                  /note=
45
                                                                                              /note- "REI Tyr-49
21.6 VL, located at
50..56
                                                                                                                                                                                                                                                                                                                                                                               /label= CDR1
/note= "21.6
35..49
                    /note- "21.6 complementarity determining region 57...88
                                                                                                                                                                                                                                                                                                       /label= fr2
/note= "REI framework region
                                                                             /label- CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-
                                                                                                                                                                                                                                                                     note- "REI Lys-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label- FR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     binding poly:peptide(s) -
therapy, e.g. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "REI framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                     REI Lys-45 is important in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 AA
                                                                                                                                                                                                                                                                                                                                                                                                      complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 63; DB 29;
Pred. No. 3.52e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       injury;
                                                                                                                              at
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                                                                                                                           is substd. by His of the binding site"
                                                                                                                                                                                                                                     substd. by supporting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapy.
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PS Claim 25; Fig 6; 107pp; English.

CC raim 25; Fig 6; 107pp; English.

CC region (VI) of a humanised alpha-4 integrin antibody 21.6. It is composed of complementarity determining regions (CDRs) from the VI.

CC region (See W22409) of mouse alpha-4 integrin monoclonal antibody 22.6 and a modified human REI framework. It can be expressed in CC mammalian host cells following PCR amplification and mutagenesis con appropriate fragments of mouse and human DNA sequences. The CC humanised 21.6 VI and a humanised 21.6 vH (see W22413) can be used to produce a claimed humanised 21.6 antibody that is useful in the CC manufacture of a medicament for treating asthma, atherosclerosis, CAIDS, dementia, diabetes, inflammatory bowel disease, rumour metastasis, nephritis, atopic dermatitis, psoriasis, myocardial constraints, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin CC may also be used in the affinity purification of alpha-4 integrin CC may also be used in the antibodies. The humanised antibody has a half-life in the human circulation essentially equivalent to that CC of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 11; Conservative
cancer diagnosis;
Synthetic.
WO9742329-A1.
                                              Anti-CEA antibody light chain variable region VK4.
Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer diagnosis; complementarity determining region; lig
                                                                                                                                    02-JUN-1998 (first entry)
                                                                                                                                                               W41390 standard; Protein; 107 W41390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bendig MM, Jones ST, Leger OJ, Saldanha J, WPI; 97-297879/27.
Uses of humanised alpha-4 integrin antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ATHE-) ATHENA NEUROSCIENCES Bendig MM, Jones ST, Leger WPI; 97-297879/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-NOV-1996; U18807.
21-NOV-1995; US-561521.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region
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                                                                                                                                                                                                                                                                                                24 MTQSPSSLSAS 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note- "REI Thr-106 substd. I of human kappa light chain J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106
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/note- "21.6
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 63; DB 24; LC
Pred. No. 3.52e+00;
"""matches 0;
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CDR2
                                                                               cancer therapy;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Tue Mar 23 15:20:39 1999; MasPar time 1.37 Seconds 34.477 Million cell updates/sec

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Description: Perfect Score: Sequence: >US-08-766-350A-4 (31-35) from US08766350A.pep (2 of 4) 31

Scoring table: PAM 150 Gap 11 1 VRSGA 5

Searched: 100342 seqs, 9469514 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Statistics: Mean 11.797; Variance 23.980; scale 0.492

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:	TELECOMMUNICATION INFORMATION:	REFERENCE/DOCKET NUMBER: C-38,///	TRATION NUMBER: 34,9	•	AGENT I	FILING DATE: 16-FEB-1993	PODITION NITHERE OR /017, 570	CENSOLFICATION DATA:	C	ž	~	SOFTWARE: PatentIn Release #1.0, Version #1.25	SYSTEM: PC-DOS/MS-DOS	COMPUTER: IBM PC compatible	_	COMPUTER READABLE FORM:	ŏ	ĸ	••	Midland	O. Box	ADDRESSEE DIANG C III ABY	NOMBEN OF BUDGESS:	TITLE OF INVENTION: ANTIGEN CHIMBRIC ANTIBODIES	OF INVENTION: A NOVEL FAMILY OF	T: SCHLOM, JEFFREY		MEZES, PETER S	RIXON,	APPLICANT: GOURLIE, BRIAN B	NFORMATION:	· m	Sequence 6, Application US/08471426		Sequence 6, Application US/08471426				XXXXX		IT 1 IS-08-471-426-6 STANDARD; PRT; 124 AA.	

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                                                                             MOLECULE TYPE: protein SEQUENCE 124 AA; 13786 MW; 91250 CN;
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                                                                                                                   TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
                                                                                                                                                          CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION UNMEER: 34,941
REFERENCE/DOCKET NUMBER: C-38
TELECOMMUNICATION INFORMATION:
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VRSGA 35
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APPLICATION NUMBER: US
FILING DATE: 19930216
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C.
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINGEMBRYONIC TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
                                                                                               TYPE: AMI
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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KAPLAN, DONALD A
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Best Local Similarity 100.0%;
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acids
TYPE: amino acids
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                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                        MOLECULE TYPE: protein JENCE 124 AA; 13786 MW; 91250 CN;
                                                                                                                                                                                                                                                                NAME: ULMER, DOANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/017,570 FILING DATE: 16-FEB-1993 ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 06-JUN-1995 CLASSIFICATION: 536
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PENTION: ANTIGEN CHIMERIC ANTIBODIES
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Sequence 6, Application PC/TUS9401709

Sequence 6, Application PC/TUS9401709